

1/117



SEQUENCE LISTING

<110> Abbott Laboratories
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<120> METHODS AND COMPOSITIONS FOR DETECTING
HEPATITIS E VIRUS

<130> 6232.US.P1

<140> US 09/468,147

<141> 1999-12-21

<150> US 09/173,141

<151> 1998-10-15

<150> US 60/061,199

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taaaatgaag gtaggtaaaa ccggggagtc ttaattaatt ccttttgtgc ccccttcgca 7140
gttctctttg gctttatttc tcatttctgc tttccgcgct ccctggaaaa aaaaaaaaaa 7200
aa

```

```

<210> 90
<211> 7202
<212> DNA
<213> Hepatitis E Virus

```

```

<220>
<223> us1full

```

```

<221> CDS
<222> (1)...(5094)
<223> Orf1

```

```

<221> CDS
<222> (5132)...(7111)
<223> Orf2

```

```

<223> Orf3 at positions 5094-5462

```

```

<223> Xaa = Unknown or Other at position 174

```

```

<223> Xaa = Unknown or Other at position 363

```

```

<223> Xaa = Unknown or Other at position 1088

```

```

<223> Xaa = Unknown or Other at position 1131

```

```

<223> Xaa = Unknown or Other at position 1217

```

```

<223> Xaa = Unknown or Other at position 1389

```

```

<223> Xaa = Unknown or Other at position 2179

```

```

<223> Xaa = Unknown or Other at position 2240

```

```

<223> Xaa = Unknown or Other at position 2293

```

```

<400> 90

```

cct ggc att act act gcc att gag cag gct gct ctg gct gcg gcc aat	48
Pro Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tct cgc gtg	96
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
caa acc gag att ctt att aat ttg atg caa ccc cgg cag ttg gtt ttc	144
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgc cct gag gta ctt tgg aat cac cct atc cag cgg gtt ata cat aat	192
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gaa tta gaa cag tac tgc cgg gct cgg gct ggt cgt tgc ttg gag gtt	240
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75 80	
gga gct cac cca aga tcc att aat gac aac ccc aac gtt ctg cat cgg	288
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
85 90 95	
tgt ttc ctt aga ccg gtt ggc cga gat gtt cag cgc tgg tac tct gcc	336
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggc cct gcg gct aat tgc cgc cgc tcc gcg ttg cgt ggt	384
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc ccc ccc gct gac cgc act tac tgc ttt gat gga ttc tcc cgt tgt	432
Leu Pro Pro Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe Ser Arg Cys	
130 135 140	
gct ttt gct gca gag acc ggt gtg gct ctt tac tct ctg cat gac ctt	480
Ala Phe Ala Ala Glu Thr Gly Val Ala Leu Tyr Ser Leu His Asp Leu	
145 150 155 160	
tgg cca gct gat gtt gca gag gct atg gcc cgc cac ggg atr aca cgc	528
Trp Pro Ala Asp Val Ala Glu Ala Met Ala Arg His Gly Xaa Thr Arg	
165 170 175	
ttg tat gcc gca ctg cac ctt ccc cct gag gtg ctg cta cca ccc ggc	576
Leu Tyr Ala Ala Leu His Leu Pro Pro Glu Val Leu Leu Pro Pro Gly	
180 185 190	
acc tac cac aca acc tcg tat ctc ctg att cac gac ggc gac cgc gct	624
Thr Tyr His Thr Thr Ser Tyr Leu Leu Ile His Asp Gly Asp Arg Ala	
195 200 205	
gtt gta act tac gag ggc gat act agt gcg ggc tat aat cat gat gtc	672
Val Val Thr Tyr Glu Gly Asp Thr Ser Ala Gly Tyr Asn His Asp Val	
210 215 220	
tcc ata ctt cgt gcg tgg atc cgt act aca aaa ata gtt ggt gat cat	720

Ser 225	Ile	Leu	Arg	Ala	Trp 230	Ile	Arg	Thr	Thr	Lys 235	Ile	Val	Gly	Asp	His 240	
ccg	ttg	gtc	ata	gag	cgt	gtg	cgg	gcc	att	gga	tgt	cat	ttt	gtg	ttg	768
Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	
				245					250					255		
ctg	ctc	acc	gca	gcc	cct	gag	ccg	tca	ccc	atg	cct	tat	gtt	cct	tac	816
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	
			260					265					270			
cct	cgt	tca	acg	gag	gtg	tat	gtc	cgg	tcc	ata	ttt	ggc	cct	ggc	ggc	864
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	
		275					280					285				
tcc	cca	tcc	ttg	ttt	ccg	tca	gcc	tgc	tct	act	aaa	tct	act	ttc	cat	912
Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	
	290					295					300					
gct	gtc	ccg	gtg	cat	atc	tgg	gat	cgg	ctc	atg	ctc	ttt	ggc	gcc	acc	960
Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr	
305					310				315						320	
ctg	gac	gat	cag	gcg	ttt	tgc	tgt	tca	cgg	ctc	atg	act	tac	ctc	cgt	1008
Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	
			325					330					335			
ggc	att	agt	tac	aag	gtc	act	gtc	ggc	gcg	ctt	gtc	gct	aat	gag	ggg	1056
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	
			340					345					350			
tgg	aac	gcc	tct	gaa	gac	gct	ctt	act	gca	rtg	atc	act	gca	gct	tat	1104
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr	
		355					360					365				
ttg	act	att	tgc	cat	cag	cgt	tat	ctc	cgc	acc	cag	gcg	ata	tcc	aag	1152
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	
		370				375					380					
ggc	atg	cgc	cgg	ttg	ggg	gtt	gag	cac	gcc	cag	aaa	ttt	atc	aca	aga	1200
Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	
385					390				395						400	
ctc	tac	agt	tgg	cta	ttt	gag	aag	tct	ggc	cgt	gat	tat	atc	ccc	ggc	1248
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	
				405					410					415		
cgc	cag	ctt	cag	ttc	tat	gca	cag	tgc	cga	cgg	tgg	cta	tct	gca	ggc	1296
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	
			420					425					430			
ttc	cac	cta	gac	ccc	agg	gta	ctt	gtt	ttt	gat	gag	tca	gta	cca	tgc	1344
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	
		435					440					445				
cgc	tgt	agg	acg	ttt	ttg	aag	aaa	gtt	gcg	ggc	aaa	ttc	tgc	tgt	ttt	1392
Arg	Cys	Arg	Thr	Phe	Leu	Lys	Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe	

450	455	460	
atg cgg tgg ctc ggg cag gag tgt acc tgc ttc ttg gag ccg gcc gag			1440
Met Arg Trp Leu Gly Gln Glu Cys Thr Cys Phe Leu Glu Pro Ala Glu			
465	470	475	480
ggt tta gtc ggc gat cat ggc cat gac aac gag gcc tat gag ggt tct			1488
Gly Leu Val Gly Asp His Gly His Asp Asn Glu Ala Tyr Glu Gly Ser			
	485	490	495
gag gtc gac ccg gct gaa cct gca cat ctt gat gtt tct ggg act tac			1536
Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser Gly Thr Tyr			
	500	505	510
gcc gtc cac ggg cac cag ctt gag gcc ctc tat agg gca ctt aat gtc			1584
Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala Leu Asn Val			
	515	520	525
cca caa gat att gcc gct cga gct tcc cga cta acg gca act gtt gag			1632
Pro Gln Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala Thr Val Glu			
	530	535	540
ctc gtt gca agt cca gac cgc tta gag tgc cgc acc gtg ctc ggt aat			1680
Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val Leu Gly Asn			
545	550	555	560
aag acc ttc cgg acg acg gtg gtc gac ggc gcc cat cta gag gcg aat			1728
Lys Thr Phe Arg Thr Thr Val Val Asp Gly Ala His Leu Glu Ala Asn			
	565	570	575
ggc cct gag cag tat gtc tta tca ttt gac gcc tcc cgt cag tct atg			1776
Gly Pro Glu Gln Tyr Val Leu Ser Phe Asp Ala Ser Arg Gln Ser Met			
	580	585	590
ggg gcc ggg tcg cat agc ctc act tat gag ctc acc cct gct ggt ttg			1824
Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro Ala Gly Leu			
	595	600	605
cag gtt agg att tca tct aat ggt ctg gat tgc act gct aca ttc ccc			1872
Gln Val Arg Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala Thr Phe Pro			
610	615	620	
ccc ggt gga gcc cct agc gct gcg ccc ggg gag gtg gca gcc ttt tgc			1920
Pro Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Ala Ala Phe Cys			
625	630	635	640
agt gcc ctt tat aga tat aac agg ttc acc cag cgg cac tcg ctg act			1968
Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His Ser Leu Thr			
	645	650	655
ggc gga tta tgg tta cac cct gag ggg ttg ctg ggt att ttc ccc cct			2016
Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile Phe Pro Pro			
	660	665	670
ttc tcc cct ggg cat atc tgg gag tct gcg aac ccc ttt tgc ggg gag			2064
Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe Cys Gly Glu			
	675	680	685

ggg act ttg tat acc cga act tgg tca aca tct ggc ttt tct agt gat	2112
Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe Ser Ser Asp	
690 695 700	
ttc tcc ccc cct gaa gcg gcc gct cct gct atg gct gct acc ccg ggg	2160
Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Met Ala Ala Thr Pro Gly	
705 710 715 720	
ctg ccc cat tct acc cca cct gtt agc gat att tgg gtg cta cca ccg	2208
Leu Pro His Ser Thr Pro Pro Val Ser Asp Ile Trp Val Leu Pro Pro	
725 730 735	
ccc tca gag gag ttt cag gtt gat gca gca cct gtg ccc cct gcc cct	2256
Pro Ser Glu Glu Phe Gln Val Asp Ala Ala Pro Val Pro Pro Ala Pro	
740 745 750	
gac cct gct gga ttg ccc ggt ccc gtt gtg ctt acc ccc ccc ccc cct	2304
Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro	
755 760 765	
ccc cct gtg cat aag cca tca ata ccc ccg cct tcc cgt aac cgt cgt	2352
Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg	
770 775 780	
ctc ctc tat acc tat cct gac ggc gct aag gtg tat gca ggg tca ctg	2400
Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu	
785 790 795 800	
ttt gaa tca gac tgt gac tgg ctg gtt aat gcc tca aac ccg ggc cat	2448
Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His	
805 810 815	
cgt ccc gga ggt ggc ctc tgc cat gcc ttt tac caa cgt ttt cca gaa	2496
Arg Pro Gly Gly Glu Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu	
820 825 830	
gcg ttt tac cca act gaa ttc atc atg cgt gag ggt ctt gca gca tac	2544
Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr	
835 840 845	
acc ttg acc ccg cgc cct atc att cat gca gtc gct ccc gat tat agg	2592
Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg	
850 855 860	
gtt gag cag aac ccg aag agg ctt gag gca gcg tac cgt gaa act tgt	2640
Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys	
865 870 875 880	
tcc cgt cgt ggc acc gct gcc tac ccg ctt ttg ggt tgc ggt ata tac	2688
Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr	
885 890 895	
cag gtc cct gtt agc ctc agt ttt gat gcc tgg gaa cgt aat cac cgc	2736
Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg	
900 905 910	

ccc ggc gat gag ctt tac ttg acc gag ccc gct gca aat tgg ttt gag	2784
Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu	
915 920 925	
gct aat aag ccg gcg cag ccg gtg ctc acc ata act gag gac acg gcc	2832
Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala	
930 935 940	
cgt acg gcc aac ctg gca ttg gag att gat gcc gct aca gag gtc ggc	2880
Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly	
945 950 955 960	
cgt gct tgt gcc ggt tgc acc atc agc cct ggc att gtg cac tat cag	2928
Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln	
965 970 975	
ttt acc gcc ggg gtc ccg ggc tcg ggc aag tca agg tcc ata caa cag	2976
Phe Thr Ala Gly Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Gln Gln	
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Gly Asp Val Asp Val Val Val Val Pro Thr Arg Glu Leu Arg Asn Ser	
995 1000 1005	
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Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro	
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cca cac ctg ttg ctg tta cat atg cag ccg gcc tcc tcg gtc cat ctc	3168
Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu	
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ctc ggt gac cca aat cag atc cct gct att gat ttt gag cac gcc ggc	3216
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly	
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ctg gtc cct gcg atc cgt ccc gag ctt gcg cca acg agc tgg tgg crc	3264
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa	
1075 1080 1085	
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Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala	
1090 1095 1100	
tac cct aaa atc cag acc acg agc cgt gtg cta ccg tcc ctg ttt tgg	3360
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp	
1105 1110 1115 1120	
aat gaa ccg gcc att ggc cag aag ttg gtt ytc acg cag gcg gca aag	3408
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys	
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Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr	
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ttc aca gag acc aca atc ata gcc acg gcc gac gcc agg ggc ctt atc	3504
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile	
1155 1160 1165	
cag tca tcc cgg gct cat gct ata gtt gca ctt act cgc cac act gag	3552
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu	
1170 1175 1180	
aag tgt gtt atc ctg gat gcc ccc ggc ctg ctt cgt gag gtc ggc att	3600
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile	
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tcg gat gtg att gtc aac aac ttt ttc ctt gct ggt ggc gag gtc ggc	3648
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly	
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crc cac cgc cct tct gtg ata cct cgc ggt aac cct gat caa aac ctc	3696
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu	
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ggg act tta cag gcc ttc ccg ccg tcc tgt caa att agt gct tac cat	3744
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His	
1235 1240 1245	
cag ttg gct gag gaa ctg ggc cat cgc ccg gcc cct gtc gcc gcc gtc	3792
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val	
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ttg ccc cct tgc cct gag ctt gag cag ggc ctg ctc tac atg cca cag	3840
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln	
1265 1270 1275 1280	
gag ctc act gtg tcc gat agt gtg ttg gtt ttt gag ctt acg gat ata	3888
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile	
1285 1290 1295	
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Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser	
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Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala	
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His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly	
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Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met	
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Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys	

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Asn	Arg	Asp	Val	Ser	Arg	Ile	Thr	Phe	Phe	Gln	Lys	Xaa	Cys	Asn	Lys	
1380				1385				1390								
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Phe	Thr	Thr	Gly	Glu	Thr	Ile	Ala	His	Gly	Lys	Val	Gly	Gln	Gly	Ile	
1395				1400				1405								
tcg	gcc	tgg	agt	aag	acc	ttc	tgc	gct	ctg	ttc	ggc	ccg	tgg	ttc	cgc	4272
Ser	Ala	Trp	Ser	Lys	Thr	Phe	Cys	Ala	Leu	Phe	Gly	Pro	Trp	Phe	Arg	
1410				1415				1420								
gcc	att	gaa	aaa	gaa	ata	ttg	gcc	ctg	ctc	ccg	cct	aat	atc	ttt	tat	4320
Ala	Ile	Glu	Lys	Glu	Ile	Leu	Ala	Leu	Leu	Pro	Pro	Asn	Ile	Phe	Tyr	
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Gly	Asp	Ala	Tyr	Glu	Glu	Ser	Val	Phe	Ala	Ala	Ala	Val	Ser	Gly	Ala	
1445				1450				1455								
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Gly	Ser	Cys	Met	Val	Phe	Glu	Asn	Asp	Phe	Ser	Glu	Phe	Asp	Ser	Thr	
1460				1465				1470								
cag	aat	aat	ttc	tct	ctt	ggc	ctt	gag	tgt	gtg	gtt	atg	gag	gag	tgc	4464
Gln	Asn	Asn	Phe	Ser	Leu	Gly	Leu	Glu	Cys	Val	Val	Met	Glu	Glu	Cys	
1475				1480				1485								
ggc	atg	cct	caa	tgg	cta	att	agg	ttg	tac	cat	ctg	gtt	cgg	tct	gcc	4512
Gly	Met	Pro	Gln	Trp	Leu	Ile	Arg	Leu	Tyr	His	Leu	Val	Arg	Ser	Ala	
1490				1495				1500								
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Trp	Ile	Leu	Gln	Ala	Pro	Lys	Glu	Ser	Leu	Lys	Gly	Phe	Trp	Lys	Lys	
1505				1510				1515				1520				
cat	tct	ggg	gag	cct	ggg	acc	ctt	ctt	tgg	aat	acc	gtc	tgg	aat	atg	4608
His	Ser	Gly	Glu	Pro	Gly	Thr	Leu	Leu	Trp	Asn	Thr	Val	Trp	Asn	Met	
1525				1530				1535								
gcg	att	ata	gca	cat	tgc	tat	gag	ttc	cgt	gac	ttt	cgt	gtt	gct	gcc	4656
Ala	Ile	Ile	Ala	His	Cys	Tyr	Glu	Phe	Arg	Asp	Phe	Arg	Val	Ala	Ala	
1540				1545				1550								
ttt	aag	ggg	gat	gat	tcg	gtg	gtc	ctc	tgt	agt	gac	tac	cga	cag	agc	4704
Phe	Lys	Gly	Asp	Asp	Ser	Val	Val	Leu	Cys	Ser	Asp	Tyr	Arg	Gln	Ser	
1555				1560				1565								
cgc	aat	gca	gct	gcc	tta	att	gct	ggc	tgt	ggg	ctc	aaa	ttg	aag	gtt	4752
Arg	Asn	Ala	Ala	Ala	Leu	Ile	Ala	Gly	Cys	Gly	Leu	Lys	Leu	Lys	Val	
1570				1575				1580								
gat	tac	cgc	cct	atc	ggg	ctg	tat	gct	ggg	gtg	gtg	gtg	gcc	ccc	ggg	4800
Asp	Tyr	Arg	Pro	Ile	Gly	Leu	Tyr	Ala	Gly	Val	Val	Val	Ala	Pro	Gly	
1585				1590				1595				1600				

ttg ggg aca ctg ccc gat gtg gtg cgt ttt gct ggt cgg ttg tct gaa Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu 1605 1610 1615	4848
aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala 1620 1625 1630	4896
gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gcg cag gtc tgt gtt Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val 1635 1640 1645	4944
gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn 1650 1655 1660	4992
ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr 1665 1670 1675 1680	5040
gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg 1685 1690 1695	5088
gtg gaa tgaataacat gtcttttgca tcgcccattgg gatcacc atg cgc cct agg Val Glu Met Arg Pro Arg 1700	5143
gct gtt ctg ttg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca Ala Val Leu Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro 1705 1710 1715	5191
ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgg cgc agc ggc ggt Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly 1720 1725 1730	5239
gcc gcc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala 1735 1740 1745 1750	5287
ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser 1755 1760 1765	5335
caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly 1770 1775 1780	5383
tcc gct tgg cgt gac cag tcc aag cgc ccc tcc gtt gcc ccc cgt cgt Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val Ala Pro Arg Arg 1785 1790 1795	5431
cga tct acc cca gct ggg gct gcg ccg cta act gcc ata tca cca gcc Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Ile Ser Pro Ala 1800 1805 1810	5479

cct gat aca gct cct gta cct gat gtt gac tca cgt ggt gct att ttg	5527
Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu	
1815 1820 1825 1830	
cgc cgg cag tac aat ttg tct acg tcc ccg ctt aca tca tct gtt gct	5575
Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala	
1835 1840 1845	
tct ggt act aat ctg gtt ctc tat gct gcc ccg ctg aac cct ctc ttg	5623
Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Asn Pro Leu Leu	
1850 1855 1860	
cct ctt cag gat ggc acc aac act cat att atg gct act gag gca tct	5671
Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser	
1865 1870 1875	
aat tac gcc cag tat cgg gtt gtt cgg gct acg att cgt tat cgc ccg	5719
Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro	
1880 1885 1890	
ttg gtg cca aat gct gtt ggt ggt tat gct atc tct att tct ttc tgg	5767
Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp	
1895 1900 1905 1910	
cct caa act aca act acc cct act tct gtt gac atg aat tct atc act	5815
Pro Gln Thr Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr	
1915 1920 1925	
tct act gat gtc agg atc ttg gtc cag ccc ggt ata gcc tcc gag tta	5863
Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu	
1930 1935 1940	
gtc atc cct agt gaa cgc ctt cac tac cgc aac caa ggc tgg cgc tct	5911
Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser	
1945 1950 1955	
gtt gag acc acg ggt gtg gcc gaa gag gag gct acc tcc ggt ctg gta	5959
Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val	
1960 1965 1970	
atg ctt tgt att cat ggc tcc cct gtt aac tcc tac act aat aca cct	6007
Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro	
1975 1980 1985 1990	
tac acc ggt gca ttg ggg ctt ctt gat ttt gca tta gaa ctt gaa ttt	6055
Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe	
1995 2000 2005	
aga aat ttg aca ccc ggg aac act aac acc cgt gtt tcc cgg tat act	6103
Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Thr	
2010 2015 2020	
agc aca gcc cgc cac cgg ctg cgc cgc ggt gct gat ggg acc gct gag	6151
Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu	
2025 2030 2035	
ctc acc acc aca gca gcc aca cgc ttc atg aag gat ttg cat ttt act	6199

Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr	
2040	2045 2050
ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg	6247
Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu	
2055	2060 2065 2070
ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att	6295
Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile	
2075	2080 2085
tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc	6343
Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala	
2090	2095 2100
aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag	6391
Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln	
2105	2110 2115
caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc	6439
Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser	
2120	2125 2130
cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct	6487
Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro	
2135	2140 2145 2150
acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat	6535
Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn	
2155	2160 2165
gat gtt ttg tgg ctc tct ctc act gcc gct gag tac grc cag acc acg	6583
Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr	
2170	2175 2180
tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt	6631
Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu	
2185	2190 2195
gtt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg	6679
Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp	
2200	2205 2210
tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat	6727
Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr	
2215	2220 2225 2230
tct aag aaa ttt tat gtt ctc ccg ctt cgs ggg aag ctg tcc ttt tgg	6775
Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp	
2235	2240 2245
gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act	6823
Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr	
2250	2255 2260
gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc	6871
Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala	

2265	2270	2275	
att tct act tat acc act agt ttg ggt gcc ggc cct acc tcg aty tct			6919
Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr Ser Xaa Ser			
2280	2285	2290	
gcg gtc ggt gta cta gct cca cat tcg gcc ctt gct gtt ctc gag gat			6967
Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp			
2295	2300	2305	2310
act gtt gat tat cct gct cgt gcc cat act ttt gat gat ttc tgc ccg			7015
Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro			
	2315	2320	2325
gag tgt cgc acc ctt ggt ctg cag ggt tgt gca ttc caa tct act att			7063
Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile			
	2330	2335	2340
gct gaa ctt cag cgt ctt aaa atg aag gta ggt aaa acc cgg gag tct			7111
Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser			
	2345	2350	2355
taattaattc cttttgtgcc cccttcgcag ttctctttgg ctttatttct catttctgct			7171
ttccgcgctc cctggaaaaa aaaaaaaaaa a			7202

<210> 91
 <211> 1698
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 174
 <223> Xaa = Unknown or Other at position 363
 <223> Xaa = Unknown or Other at position 1088
 <223> Xaa = Unknown or Other at position 1131
 <223> Xaa = Unknown or Other at position 1217
 <223> Xaa = Unknown or Other at position 1389

<400> 91															
Pro	Gly	Ile	Thr	Ala	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	
1			5				10					15			
Ser	Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val
		20					25					30			
Gln	Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe
		35				40						45			
Arg	Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn
	50				55				60						
Glu	Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val
65				70					75					80	
Gly	Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg
			85				90						95		
Cys	Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala

			100					105					110		
Pro	Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly
		115					120					125			
Leu	Pro	Pro	Ala	Asp	Arg	Thr	Tyr	Cys	Phe	Asp	Gly	Phe	Ser	Arg	Cys
	130					135					140				
Ala	Phe	Ala	Ala	Glu	Thr	Gly	Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu
145					150					155					160
Trp	Pro	Ala	Asp	Val	Ala	Glu	Ala	Met	Ala	Arg	His	Gly	Xaa	Thr	Arg
			165						170					175	
Leu	Tyr	Ala	Ala	Leu	His	Leu	Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly
			180					185					190		
Thr	Tyr	His	Thr	Thr	Ser	Tyr	Leu	Leu	Ile	His	Asp	Gly	Asp	Arg	Ala
		195					200					205			
Val	Val	Thr	Tyr	Glu	Gly	Asp	Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val
	210					215					220				
Ser	Ile	Leu	Arg	Ala	Trp	Ile	Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His
225					230					235					240
Pro	Leu	Val	Ile	Glu	Arg	Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu
				245					250					255	
Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr
			260					265					270		
Pro	Arg	Ser	Thr	Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly
			275				280					285			
Ser	Pro	Ser	Leu	Phe	Pro	Ser	Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His
	290					295					300				
Ala	Val	Pro	Val	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr
305					310					315					320
Leu	Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg
				325					330					335	
Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly
			340					345					350		
Trp	Asn	Ala	Ser	Glu	Asp	Ala	Leu	Thr	Ala	Xaa	Ile	Thr	Ala	Ala	Tyr
	355						360					365			
Leu	Thr	Ile	Cys	His	Gln	Arg	Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys
	370					375					380				
Gly	Met	Arg	Arg	Leu	Gly	Val	Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg
385					390					395					400
Leu	Tyr	Ser	Trp	Leu	Phe	Glu	Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly
				405					410					415	
Arg	Gln	Leu	Gln	Phe	Tyr	Ala	Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly
			420					425					430		
Phe	His	Leu	Asp	Pro	Arg	Val	Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys
		435													

Lys	Thr	Phe	Arg	Thr	Thr	Val	Val	Asp	Gly	Ala	His	Leu	Glu	Ala	Asn	
				565					570					575		
Gly	Pro	Glu	Gln	Tyr	Val	Leu	Ser	Phe	Asp	Ala	Ser	Arg	Gln	Ser	Met	
			580					585					590			
Gly	Ala	Gly	Ser	His	Ser	Leu	Thr	Tyr	Glu	Leu	Thr	Pro	Ala	Gly	Leu	
		595					600					605				
Gln	Val	Arg	Ile	Ser	Ser	Asn	Gly	Leu	Asp	Cys	Thr	Ala	Thr	Phe	Pro	
	610					615					620					
Pro	Gly	Gly	Ala	Pro	Ser	Ala	Ala	Pro	Gly	Glu	Val	Ala	Ala	Phe	Cys	
625					630					635					640	
Ser	Ala	Leu	Tyr	Arg	Tyr	Asn	Arg	Phe	Thr	Gln	Arg	His	Ser	Leu	Thr	
			645					650						655		
Gly	Gly	Leu	Trp	Leu	His	Pro	Glu	Gly	Leu	Leu	Gly	Ile	Phe	Pro	Pro	
		660						665					670			
Phe	Ser	Pro	Gly	His	Ile	Trp	Glu	Ser	Ala	Asn	Pro	Phe	Cys	Gly	Glu	
	675						680					685				
Gly	Thr	Leu	Tyr	Thr	Arg	Thr	Trp	Ser	Thr	Ser	Gly	Phe	Ser	Ser	Asp	
	690					695					700					
Phe	Ser	Pro	Pro	Glu	Ala	Ala	Ala	Pro	Ala	Met	Ala	Ala	Thr	Pro	Gly	
705					710					715					720	
Leu	Pro	His	Ser	Thr	Pro	Pro	Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro	
			725						730					735		
Pro	Ser	Glu	Glu	Phe	Gln	Val	Asp	Ala	Ala	Pro	Val	Pro	Pro	Ala	Pro	
		740						745					750			
Asp	Pro	Ala	Gly	Leu	Pro	Gly	Pro	Val	Val	Leu	Thr	Pro	Pro	Pro	Pro	
	755						760					765				
Pro	Pro	Val	His	Lys	Pro	Ser	Ile	Pro	Pro	Pro	Ser	Arg	Asn	Arg	Arg	
	770					775						780				
Leu	Leu	Tyr	Thr	Tyr	Pro	Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu	
785				790					795						800	
Phe	Glu	Ser	Asp	Cys	Asp	Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His	
			805						810					815		
Arg	Pro	Gly	Gly	Gly	Leu	Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu	
		820						825					830			
Ala	Phe	Tyr	Pro	Thr	Glu	Phe	Ile	Ile	Met	Arg	Glu	Gly	Leu	Ala	Tyr	
	835						840					845				
Thr	Leu	Thr	Pro	Arg	Pro	Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg	
	850					855						860				
Val	Glu	Gln	Asn	Pro	Lys	Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys	
865				870					875						880	
Ser	Arg	Arg	Gly	Thr	Ala	Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr	
			885						890					895		
Gln	Val	Pro	Val	Ser	Leu	Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg	
		900						905					910			
Pro	Gly	Asp	Glu	Leu	Tyr	Leu	Thr	Glu	Pro	Ala	Ala	Asn	Trp	Phe	Glu	
		915					920					925				
Ala	Asn	Lys	Pro	Ala	Gln	Pro	Val	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala	
	930					935					940					
Arg	Thr	Ala	Asn	Leu	Ala	Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly	
945				950					955						960	
Arg	Ala	Cys	Ala	Gly	Cys	Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln	
			965						970					975		
Phe	Thr	Ala	Gly	Val	Pro	Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln	
		980						985					990			
Gly	Asp	Val	Asp	Val	Val	Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser	
	995						1000					1005				
Trp	Arg	Arg	Arg	Gly	Phe	Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg	

1010		1015		1020
Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro				
1025		1030		1035
Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu				1040
		1045		1050
Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly				1055
		1060		1065
Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa				1070
		1075		1080
Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala				1085
		1090		1095
Tyr Pro Lys Ile Gln Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp				1100
1105		1110		1115
Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys				1120
		1125		1130
Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr				1135
		1140		1145
Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile				1150
		1155		1160
Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu				1165
		1170		1175
Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile				1180
1185		1190		1195
Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly				1200
		1205		1210
Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu				1215
		1220		1225
Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His				1230
		1235		1240
Gln Leu Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val				1245
		1250		1255
Leu Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln				1260
1265		1270		1275
Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile				1280
		1285		1290
Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val Leu Ser				1295
		1300		1305
Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala				1310
		1315		1320
His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly				1325
		1330		1335
Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met				1340
1345		1350		1355
Val Glu Lys Gly Gln Asp Gly Ser Ala Val Leu Glu Leu Asp Leu Cys				1360
		1365		1370
Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys				1375
		1380		1385
Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile				1390
		1395		1400
Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg				1405
		1410		1415
Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr				1420
1425		1430		1435
Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Val Ser Gly Ala				1440
		1445		1450
Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr				1455
		1460		1465
				1470

Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys
 1475 1480 1485
 Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala
 1490 1495 1500
 Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys
 1505 1510 1515 1520
 His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met
 1525 1530 1535
 Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala
 1540 1545 1550
 Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser
 1555 1560 1565
 Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val
 1570 1575 1580
 Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly
 1585 1590 1595 1600
 Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu
 1605 1610 1615
 Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala
 1620 1625 1630
 Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val
 1635 1640 1645
 Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn
 1650 1655 1660
 Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr
 1665 1670 1675 1680
 Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg
 1685 1690 1695
 Val Glu

<210> 92
 <211> 660
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 481
 <223> Xaa = Unknown or Other at position 542
 <223> Xaa = Unknown or Other at position 595

<400> 92
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 Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg
 20 25 30
 Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser
 35 40 45
 Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala
 50 55 60
 Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro
 65 70 75 80
 Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val
 85 90 95
 Ala Pro Arg Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala

			100					105					110		
Ile	Ser	Pro	Ala	Pro	Asp	Thr	Ala	Pro	Val	Pro	Asp	Val	Asp	Ser	Arg
		115					120					125			
Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	Thr
	130					135					140				
Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	Leu
145					150					155					160
Asn	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	Ala
				165					170					175	
Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Val	Arg	Ala	Thr	Ile
			180					185					190		
Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	Ser
		195					200					205			
Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	Met
	210					215					220				
Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	Ile
225					230					235					240
Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	Gln
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Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	Ala	Thr
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Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	Tyr
		275					280					285			
Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	Leu
		290				295					300				
Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	Val
305					310					315					320
Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	Asp
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Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp
			340					345					350		
Leu	His	Phe	Thr	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile
		355					360					365			
Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro
		370				375					380				
Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro
385					390					395					400
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
				405					410						415
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp
			420					425					430		
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40/117

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<212> PRT
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Gly	Leu	Phe	Cys 20	Cys	Cys	Ser	Ser	Cys 25	Phe	Cys	Leu	Cys	Cys 30	Pro	Arg	
His	Arg	Pro	Val 35	Ser	Arg	Leu	Ala 40	Val	Ala	Val	Gly 45	Gly	Ala	Ala	Ala	
Val	Pro 50	Ala	Val	Val	Ser	Gly 55	Val	Thr	Gly	Leu 60	Ile	Leu	Ser	Pro	Ser	
Pro 65	Ser	Pro	Ile	Phe 70	Ile	Gln	Pro	Thr	Pro	Ser 75	Pro	Pro	Met	Ser	Phe 80	
His	Asn	Pro	Gly 85	Leu	Glu	Leu	Ala	Leu	Asp 90	Ser	Arg	Pro	Ala 95	Pro	Ser	
Val	Pro	Leu	Gly 100	Val	Thr	Ser	Pro	Ser 105	Ala	Pro	Pro	Leu 110	Pro	Pro	Val	
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<213> Artificial Sequence
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<213> Artificial Sequence

<220>
<223> Primer US5P296A

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<210> 97
<211> 20
<212> DNA
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<220>
<223> Primer US5P243A/20

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<210> 98
<211> 199
<212> DNA
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tcacacctac cagcgggtta tacataatga attagagcag tactgccggg cccgggctgg      180
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<220>
<223> JE orf1-s

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<210> 100
<211> 26
<212> DNA
<213> Hepatitis E Virus

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<220>

<223> JE orf1-a

<400> 100

gaatcaggag atacgaggtt gtgtgg

26

<210> 101

<211> 331

<212> DNA

<213> Hepatitis E Virus

<220>

<223> us2-320

<400> 101

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gaccgcacct	attgttttga	tggattttcc	cggtgtgctt	ttgctgcaga	gaccggtgtg	180
gccctttact	ctttgcatga	cctttggcca	gctgatgttg	cagaggctat	ggcccgccat	240
gggatgacac	gcttatacgc	cgcactgcac	cttccccccg	aggtgctgct	accacccggc	300
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<210> 102

<211> 1186

<212> DNA

<213> Hepatitis E Virus

<220>

<223> us2-1168

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actaaattat	atgaggcggc	gcattcagat	gtccgtgagt	ccctagcgag	gtttatcccc	180
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cgcatcacat	ttttccaaaa	ggattgcaat	aagtttacia	ctggtgagac	tatcgcccat	360
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gacgcctatg	aggagtcagt	gtttgctgcc	gctgtgtccg	gggcaggggc	atgtatggta	540
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<210> 103

<211> 23

<212> DNA

<213> Hepatitis E Virus

<220>
 <223> JE hevdf2/3 s1

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 gttccgcttg gcgtgaccag tcc 23

 <210> 104
 <211> 23
 <212> DNA
 <213> Hepatitis E virus

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 <223> JE hevdf2/3 a1

 <400> 104
 gagtcaacat caggtacagg agc 23

 <210> 105
 <211> 130
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> us2-135

 <400> 105
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 atgttgactc 130

 <210> 106
 <211> 26
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> JE hevdf1-s1

 <400> 106
 gatgtcattt tgtgttgctg ctcacc 26

 <210> 107
 <211> 23
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> hev216 a1

 <400> 107
 cgtcctacag cggcatggta ctg 23

 <210> 108
 <211> 564
 <212> DNA
 <213> Hepatitis E Virus

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<223> us2-563

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gctgtcccg	ttcacatctg	ggatcrgctc	atgctctttg	gtgccaccct	gracgatcag	180
gcgttctgct	gttcacggct	tatgacttac	ctccgtggta	ttagttataa	ggtcactgtc	240
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actgcggcct	atctgacccat	ctgccatcag	cgttaccttc	gcacccaggc	gatttccaag	360
ggcatgcgcc	ggttggagg	tgagcatgct	cagaaattta	tcacaagact	ctacagctgg	420
ctatttgaga	agtctggccg	tgactacatc	cccggccgcc	agcttcaatt	ttatgcacaa	480
tgccgacggt	ggctttctgc	aggcttccac	ctaracccca	gggtgcttgt	ctttgatgaa	540
tcagtaccat	gocgctgtag	gacg				564

<210> 109

<211> 24

<212> DNA

<213> Hepatitis E Virus

<220>

<223> USorf2.1'

<400> 109

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<210> 110

<211> 678

<212> DNA

<213> Hepatitis E Virus

<220>

<223> us2-667

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atgcgcagca	agacaagggc	atcaccattc	cacatgatat	agacctgggt	gactcccgtg	180
tggttatcca	ggattatgat	aaccagcayg	agcaagaccg	acctactccg	tcacctgccc	240
cctctcgccc	cttctcagtt	cttcgtgcca	atgatgtttt	gtggctttcc	ctcactgccc	300
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ttacgcttgt	taatgtggct	actggtgctc	aggctgttgc	ccgctccctt	gattgggtcta	420
aagttactct	ggacggccgc	ccccttacta	ccattcagca	gtattctaag	acattttatg	480
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cttacaatta	taatactacc	gctagtgacc	aaattttgat	tgagaatgcg	gccggccacc	600
gtgtcgctat	ttccacctat	accactagct	taggtgccgg	tcctacctcg	atctctgcgg	660
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<210> 111

<211> 23

<212> DNA

<213> Hepatitis E Virus

<220>

<223> hev3301s

<400> 111
 gtatgcgagc tcatccgtgg tgc 23

 <210> 112
 <211> 25
 <212> DNA
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 <220>
 <223> JE hev167-a1

 <400> 112
 ccaacacact atcggacaca gtgag 25

 <210> 113
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 <212> DNA
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 gctgccaacc ctggtgcatg tacggttcac gaagctcagg gtgctacttt cacggagacc 180
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 gtgcgactca ccgcgcatac tgagaagtgt gttattttgg atgcccccg cttgttgccg 300
 gaggtcggca tttcggatgt tattgtcaat aactttttcc ttgccgggtg agaggtcggc 360
 catcacccgc cttctgtgat acctcgcggc aatcctgac agaacctcg gactctacag 420
 gcctttccgc cgtcatgtca gatcagtgtc taccatcagt tggctgagga actaggtcat 480
 cgcccgggcc ctgtcgccgc cgtcttgccc ccttgccctg agcttgagca gggcctgctc 540
 tatatgccac aagaactcac tgtgtccgat agtgtgttgg 580

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 <211> 26
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> HEV459 s1

 <400> 114
 cagaaattta tcacaagact ctacag 26

 <210> 115
 <211> 26
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 <220>
 <223> HEV459 s3

 <400> 115
 ctctacagtt ggctatttga gaagtc 26

 <210> 116

<211> 25
 <212> DNA
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<220>
 <223> JE1955a

<400> 116
 ctataaagag ctgagcagaa ggcg

25

<210> 117
 <211> 734
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2-733

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 gtctttgatg aatcagtgcc atgccgttgc aggacgtttt tgaagaaggt cgcgggtaaa 180
 ttctgctgtt ttatgcggtg gctggggcag gagtgtacct gcttcttgga gccagccgag 240
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 tatgtttctgt catttgacgc ctctcgccag tctatggggg ccgggtcgca cagcctcact 600
 tatgagctca cccctgccgg tctgcaggtg aagatttcat ctaatggtct ggattgcact 660
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 tcagctcttt atag 734

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 <212> DNA
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<220>
 <223> JE 2950mex s

<400> 118
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22

<210> 119
 <211> 22
 <212> DNA
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<220>
 <223> JE us2-579-a2

<400> 119
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22

<210> 120
 <211> 483

<212> DNA
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 caccgcacct gctgctgtta cacatgcagc gggcctcctc ggtccatctc cttggtgatc 240
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 tcatacgtgg ggcctacccc aaaattcaga ccacgagccg tgtgctacgg tccctgtttt 420
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 <211> 24
 <212> DNA
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 <220>
 <223> JE 2600s

 <400> 121
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 <210> 122
 <211> 22
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 <220>
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 <210> 123
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 <210> 124
 <211> 431
 <212> DNA
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<400> 124
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 aagggtccata caacagggag atgtcgatgt ggtgggtgtg cccacccggg agtcccgtaa 420
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 <211> 22
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2-orf2/3 s1

<400> 125
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<210> 126
 <211> 25
 <212> DNA
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<220>
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<400> 126
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<210> 127
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 <212> DNA
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<400> 127
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<212> DNA
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<210> 130
 <211> 24
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2 330s1

<400> 130
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<210> 131
 <211> 24
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2 563a1

<400> 131
 gcaggctgat ggaaacaagg atgg 24

<210> 132
 <211> 407
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2-406

<400> 132
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tggtcataga	gcgagtgcgg	gccattgggt	gtcattttgt	gctgctgctc	accgcagccc	300
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<220>
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 <211> 23
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> us2-1168 a1

<400> 134		
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<210> 135
 <211> 22
 <212> DNA
 <213> Hepatitis E Virus

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<210> 164
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<223> orf1

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<223> orf3 at positions 5159-5527

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<223> Xaa = Unknown or Other at position 331

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Ile Lys Ala Pro Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Ala	
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gcg gct aat tcc gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt ctt	149
Ala Ala Asn Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu	
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tct cgt gtg caa act gag att ctt att aat ttg atg caa ccc cgg cag	197
Ser Arg Val Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln	
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Leu Val Phe Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val	
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Ile His Asn Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys	
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His	Asp	Leu	Trp	Pro	Ala	Asp	Val	Ala	Glu	Ala	Met	Ala	Arg	His	Gly	
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Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu	Pro	Pro	Glu	Val	Leu	Leu	
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Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	
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Thr	Phe	His	Ala	Val	Pro	Val	His	Ile	Trp	Asp	Xaa	Leu	Met	Leu	Phe	
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Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr	Val	Gly	Ala	Leu	Val	Ala	
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Pro Asp Tyr Arg Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr	
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ctc	gac	ctt	tgc	aat	cgt	gac	gtc	tgc	cgc	atc	aca	ttt	ttc	caa	aag								
Leu	Asp	Leu	Cys	Asn	Arg	Asp	Val	Ser	Arg	Ile	Thr	Phe	Phe	Gln	Lys								
		1385					1390					1395											
gat	tgc	aat	aag	ttt	aca	act	ggt	gag	act	atc	gcc	cat	ggc	aag	gtt								
Asp	Cys	Asn	Lys	Phe	Thr	Thr	Gly	Glu	Thr	Ile	Ala	His	Gly	Lys	Val								
		1400					1405				1410												
ggc	cag	ggc	ata	tgc	gcc	tgg	agc	aag	acc	ttc	tgt	gct	ctg	ttt	ggc								
Gly	Gln	Gly	Ile	Ser	Ala	Trp	Ser	Lys	Thr	Phe	Cys	Ala	Leu	Phe	Gly								
		1415				1420				1425				1430									
ccg	tgg	ttc	cgc	gcc	att	gaa	aag	gaa	ata	ttg	gcc	cta	ctc	ccg	cct								
Pro	Trp	Phe	Arg	Ala	Ile	Glu	Lys	Glu	Ile	Leu	Ala	Leu	Leu	Pro	Pro								
			1435						1440					1445									
aat	atc	ttt	tat	ggc	gac	gcc	tat	gag	gag	tca	gtg	ttt	gct	gcc	gct								
Asn	Ile	Phe	Tyr	Gly	Asp	Ala	Tyr	Glu	Glu	Ser	Val	Phe	Ala	Ala	Ala								
		1450						1455				1460											
gtg	tcc	ggg	gca	ggg	tca	tgt	atg	gta	ttt	gaa	aat	gac	ttc	tca	gag								
Val	Ser	Gly	Ala	Gly	Ser	Cys	Met	Val	Phe	Glu	Asn	Asp	Phe	Ser	Glu								
		1465					1470					1475											
ttt	gac	agt	acc	cag	aat	aat	ttc	tct	ctc	ggc	ctt	gag	tgt	gtg	gtt								
Phe	Asp	Ser	Thr	Gln	Asn	Asn	Phe	Ser	Leu	Gly	Leu	Glu	Cys	Val	Val								
		1480					1485				1490												
atg	gag	gag	tgc	ggc	atg	ccc	caa	tgg	tta	att	agg	ttg	tac	cat	ctg								
Met	Glu	Glu	Cys	Gly	Met	Pro	Gln	Trp	Leu	Ile	Arg	Leu	Tyr	His	Leu								
		1495				1500				1505					1510								

gtc cgg tca gcc tgg att ttg cag gcg ccg aag gag tct ctt aag ggg	4613
Val Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly	
1515 1520 1525	
ttt tgg aag aag cac tct ggt gag cct ggt acc ctt ctc tgg aac act	4661
Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr	
1530 1535 1540	
gtc tgg aac atg gcg att ata gca cat tgc tay gag ttc cgt gac ttt	4709
Val Trp Asn Met Ala Ile Ile Ala His Cys Xaa Glu Phe Arg Asp Phe	
1545 1550 1555	
cgt gtt gcc gcc ttc aag ggt gat gat tca gtg gtc ctc tgt agt gac	4757
Arg Val Ala Ala Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp	
1560 1565 1570	
tac cga cag rgc cgt aac gcg gct gcc tta att gca ggc tgt ggg ctc	4805
Tyr Arg Gln Xaa Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu	
1575 1580 1585 1590	
aaa ttg aag gtt gat tac cgc cct atc ggg cta tat gct gga gtg gtg	4853
Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val	
1595 1600 1605	
gtg gcc ccc ggt ttg ggg aca ctg ccc gat gtg gtg cgt ttt gcc ggt	4901
Val Ala Pro Gly Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly	
1610 1615 1620	
cgg tta tct gag aag aat tgg ggc cct ggc ccg gag cgt gct gag cag	4949
Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln	
1625 1630 1635	
ctg cgt ctt gct gtt tgt gat ttc ctt cga ggg ttg acg aat gtt gcg	4997
Leu Arg Leu Ala Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala	
1640 1645 1650	
cag gtc tgt gtt gat gtt gtg tcc cgt gtc tat gga gtt agc ccc ggg	5045
Gln Val Cys Val Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly	
1655 1660 1665 1670	
ctg gta cat aac ctt att ggc atg ctg cag acc att gct gat ggc aag	5093
Leu Val His Asn Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys	
1675 1680 1685	
gcc cac ttt aca gar aat att aaa cct gtg ctt gac ctt aca aat tcc	5141
Ala His Phe Thr Xaa Asn Ile Lys Pro Val Leu Asp Leu Thr Asn Ser	
1690 1695 1700	
atc ata caa cgg gtg gaa tgaataacat gtcttttgca tcgccccatgg	5189
Ile Ile Gln Arg Val Glu	
1705	
gatcacc atg cgc cct agg gct gtt ctg ttg ttg ctc ttc gtg ctt ttg	5238
Met Arg Pro Arg Ala Val Leu Leu Leu Leu Phe Val Leu Leu	
1710 1715 1720	

cct atg ctg ccc gcg cca ccg gcc ggc cag ccg tct ggc cgc cgt cgt	5286
Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg	
1725 1730 1735	
ggg cgg cgc agc ggc ggt gcc ggc ggt ggt ttc tgg ggt gac agg gtt	5334
Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Gly Asp Arg Val	
1740 1745 1750	
gat tct cag ccc ttc gcc ctc ccc tat att cat cca acc aac ccc ttc	5382
Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro Phe	
1755 1760 1765 1770	
gcc gcc gat gtc gtt tca caa ccc ggg gct gga act cgc cct cga cag	5430
Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln	
1775 1780 1785	
ccg ccc cgc ccc ctt ggy tcc gct tgg cgt gac cag tcc cag cgc ccc	5478
Pro Pro Arg Pro Leu Xaa Ser Ala Trp Arg Asp Gln Ser Gln Arg Pro	
1790 1795 1800	
tcc gct gcc ccc cgt cgt cga tct gcc cca gct ggg gct gcg ccg ctg	5526
Ser Ala Ala Pro Arg Arg Arg Ser Ala Pro Ala Gly Ala Ala Pro Leu	
1805 1810 1815	
act gcc gtg tca ccg gct cct gac aca gcc cct gta cct gat gtt gac	5574
Thr Ala Val Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val Asp	
1820 1825 1830	
tca cgt ggt gct att ctg cgc cgg cag tac aat ttg tcc acg tcc ccg	5622
Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro	
1835 1840 1845 1850	
ctc acg tca tct gtc gct tgc ggt act aat ttg gtc ctc tat gct gcc	5670
Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala	
1855 1860 1865	
ccg ctg aat ccc ctc ttg cct ctc cag gat ggt acc aac act cat att	5718
Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile	
1870 1875 1880	
atg gct act gag gca tcc aat tat gcc cag tat ccg gtt gtt cga gct	5766
Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala	
1885 1890 1895	
aca atc cgt tat cgc ccg ctg gtg ccg aat gcc gtt ggt ggc tat gcc	5814
Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala	
1900 1905 1910	
att tcc att tct ttc tgg ccc caa act aca act acc cct act tct gtc	5862
Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val	
1915 1920 1925 1930	
gat atg aat tct att act tcc acy gat gtt agg att ttg gtt cag ccc	5910
Asp Met Asn Ser Ile Thr Ser Xaa Asp Val Arg Ile Leu Val Gln Pro	
1935 1940 1945	
ggt att gcc tcc gag cta gtc atc ccc agt gag cgc ctt cat tac cgt	5958

Gly	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	
			1950					1955					1960			
aat	caa	ggc	tgg	cgc	tct	gtt	gag	acc	acg	ggg	gtg	gct	gag	gag	gag	6006
Asn	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	
		1965					1970					1975				
gct	act	tcc	ggg	ctg	gta	atg	ctt	tgc	att	cat	ggc	tct	cct	gtt	aat	6054
Ala	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	
	1980					1985					1990					
tcc	tac	act	aat	aca	cct	tac	act	ggg	gcg	ctg	ggg	ctt	ctt	gat	ttt	6102
Ser	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	
1995					2000					2005					2010	
gca	cta	gag	ctt	gaa	ttt	agg	aat	ttg	aca	ccc	ggg	aac	acc	aac	acc	6150
Ala	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	
				2015					2020					2025		
cgt	gtt	tcc	cgg	tat	acc	agc	aca	gcc	cgc	cac	cgg	ctg	cgc	cgt	ggg	6198
Arg	Val	Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	
			2030					2035				2040				
gct	gat	ggg	act	gct	gag	ctt	act	acc	aca	gca	gcc	aca	cgt	ttc	atg	6246
Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	
		2045					2050					2055				
aag	gac	ctg	cac	ttc	gct	ggc	acg	aat	ggc	gtt	ggg	gag	gtg	ggg	cgt	6294
Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	
	2060					2065					2070					
ggg	atc	gcc	ctg	aca	ctg	ttc	aat	ctc	gct	gat	acg	ctt	ctc	ggc	ggg	6342
Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	
2075					2080					2085					2090	
tta	ccg	aca	gaa	ttg	att	tcg	tcg	gct	ggg	ggc	caa	ctg	ttt	tac	tcc	6390
Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	
				2095					2100					2105		
cgc	ccg	gtt	gtc	tca	gcc	aat	ggc	gag	cca	aca	gta	aag	tta	tat	aca	6438
Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	
				2110				2115					2120			
tct	gtt	gag	aat	gcg	cag	caa	gac	aag	ggc	atc	acc	att	cca	cat	gat	6486
Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	
		2125					2130					2135				
ata	gac	ctg	ggg	gac	tcc	cgt	gtg	gtt	atc	cag	gat	tat	gat	aac	cag	6534
Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	
	2140					2145					2150					
cay	gag	caa	gac	cga	cct	act	ccg	tca	cct	gcc	ccc	tct	cgc	ccc	ttc	6582
Xaa	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	
2155					2160					2165					2170	
tca	gtt	ctt	cgt	gcc	aat	gat	gtt	ttg	tgg	ctt	tcc	ctc	act	gcc	gct	6630
Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	

70/117

2175	2180	2185	
gag tat gac cag act acg tat ggg tcg tcc acc aac cct atg tat gtc Glu Tyr Asp Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val 2190 2195 2200			6678
tct gac aca gtt acg ctt gtt aat gtg gct act ggt gct cag gct gtt Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val 2205 2210 2215			6726
gcc cgc tcc ctt gat tgg tct aaa gtt act ctg gac ggc cgc ccc ctt Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu 2220 2225 2230			6774
act acc att cag cag tat tct aag aca ttt tat gtt ctc ccg ctc cgc Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg 2235 2240 2245 2250			6822
ggg aag ctg tcc ttt tgg gag gct ggc acg act aag gcc ggc tac cct Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro 2255 2260 2265			6870
tac aat tat aat act acc gct agt gac caa att ttg att gag aat gcg Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala 2270 2275 2280			6918
gcc ggc cac cgt gtc gct att tcc acc tat acc act agc tta ggt gcc Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala 2285 2290 2295			6966
ggt cct acc tcg atc tct gcg gtc ggc gta ctg gct cca cac tct gcc Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala 2300 2305 2310			7014
ctt gcc gtt ctt gag gat act att gat tac ccc gcc cgt gcc cat act Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr 2315 2320 2325 2330			7062
ttt gat gat ttt tgc ccg gag tgc cgt acc cta ggt ttg cag ggt tgt Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys 2335 2340 2345			7110
gca ttc cag tct act att gct gag ctc cag cgt tta aaa atg aag gta Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val 2350 2355 2360			7158
ggt aaa acc cgg gag tct taattaattc cttctgtgcc cccttcgtag Gly Lys Thr Arg Glu Ser 2365			7206
tttcttttcgc ttttattttct tattttctgct ttccgcgctc cctggaaaaa aaaaaaaaaa aaaaaaaaaa a			7266 7277

<210> 166
 <211> 1708
 <212> PRT
 <213> Hepatitis E Virus

<220>

<223> Xaa = Unknown or Other at position 322

<223> Xaa = Unknown or Other at position 331

<223> Xaa = Unknown or Other at position 445

<223> Xaa = Unknown or Other at position 448

<223> Xaa = Unknown or Other at position 634

<223> Xaa = Unknown or Other at position 646

<223> Xaa = Unknown or Other at position 811

<223> Xaa = Unknown or Other at position 1553

<223> Xaa = Unknown or Other at position 1578

<223> Xaa = Unknown or Other at position 1691

<400> 166

Met	Glu	Ala	His	Gln	Phe	Ile	Lys	Ala	Pro	Gly	Ile	Thr	Thr	Ala	Ile
1				5					10					15	
Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser	Ala	Leu	Ala	Asn	Ala	Val
			20					25					30		
Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	Gln	Thr	Glu	Ile	Leu	Ile	Asn
		35					40					45			
Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg	Pro	Glu	Val	Leu	Trp	Asn
	50					55					60				
His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	Leu	Glu	Gln	Tyr	Cys	Arg
65				70					75						80
Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly	Ala	His	Pro	Arg	Ser	Ile
			85						90					95	
Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys	Phe	Leu	Arg	Pro	Val	Gly
			100					105					110		
Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro	Thr	Arg	Gly	Pro	Ala	Ala
		115					120					125			
Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu	Pro	Pro	Val	Asp	Arg	Thr
		130				135					140				
Tyr	Cys	Phe	Asp	Gly	Phe	Ser	Arg	Cys	Ala	Phe	Ala	Ala	Glu	Thr	Gly
145				150					155						160
Val	Ala	Leu	Tyr	Ser	Leu	His	Asp	Leu	Trp	Pro	Ala	Asp	Val	Ala	Glu
			165					170					175		
Ala	Met	Ala	Arg	His	Gly	Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu
			180					185					190		
Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly	Thr	Tyr	His	Thr	Thr	Ser	Tyr
		195					200					205			
Leu	Leu	Ile	His	Asp	Gly	Asn	Arg	Ala	Val	Val	Thr	Tyr	Glu	Gly	Asp
		210				215					220				
Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val	Ser	Ile	Leu	Arg	Ala	Trp	Ile
225				230						235					240
Arg	Thr	Thr	Lys	Ile	Val	Gly	Asp	His	Pro	Leu	Val	Ile	Glu	Arg	Val
			245						250					255	
Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu
			260					265					270		

Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	Pro	Arg	Ser	Thr	Glu	Val	Tyr
		275					280					285			
Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	Ser	Pro	Ser	Leu	Phe	Pro	Ser
	290					295				300					
Ala	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	Ala	Val	Pro	Val	His	Ile	Trp
305					310					315					320
Asp	Xaa	Leu	Met	Leu	Phe	Gly	Ala	Thr	Leu	Xaa	Asp	Gln	Ala	Phe	Cys
			325						330					335	
Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr
		340						345					350		
Val	Gly	Ala	Leu	Val	Ala	Asn	Glu	Gly	Trp	Asn	Ala	Ser	Glu	Asp	Ala
		355					360					365			
Leu	Thr	Ala	Val	Ile	Thr	Ala	Ala	Tyr	Leu	Thr	Ile	Cys	His	Gln	Arg
	370					375					380				
Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	Gly	Met	Arg	Arg	Leu	Glu	Val
385					390					395					400
Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	Leu	Tyr	Ser	Trp	Leu	Phe	Glu
			405						410					415	
Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	Arg	Gln	Leu	Gln	Phe	Tyr	Ala
			420					425					430		
Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	Phe	His	Leu	Xaa	Pro	Arg	Xaa
		435					440					445			
Leu	Val	Phe	Asp	Glu	Ser	Val	Pro	Cys	Arg	Cys	Arg	Thr	Phe	Leu	Lys
	450					455				460					
Lys	Val	Ala	Gly	Lys	Phe	Cys	Cys	Phe	Met	Arg	Trp	Leu	Gly	Gln	Glu
465					470					475					480
Cys	Thr	Cys	Phe	Leu	Glu	Pro	Ala	Glu	Gly	Leu	Val	Gly	Asp	Gln	Gly
			485						490					495	
His	Asp	Asn	Glu	Ala	Tyr	Glu	Gly	Ser	Glu	Val	Asp	Pro	Ala	Glu	Pro
		500						505					510		
Ala	His	Leu	Asp	Val	Ser	Gly	Thr	Tyr	Ala	Val	His	Gly	His	Gln	Leu
		515					520					525			
Glu	Ala	Leu	Tyr	Arg	Ala	Leu	Asn	Val	Pro	His	Asp	Ile	Ala	Ala	Arg
	530					535				540					
Ala	Ser	Arg	Leu	Thr	Ala	Thr	Val	Glu	Leu	Val	Ala	Ser	Pro	Asp	Arg
545					550					555					560
Leu	Glu	Cys	Arg	Thr	Val	Leu	Gly	Asn	Lys	Thr	Phe	Arg	Thr	Thr	Val
			565					570						575	
Val	Asp	Gly	Ala	His	Leu	Glu	Ala	Asn	Gly	Pro	Glu	Glu	Tyr	Val	Leu
		580						585					590		
Ser	Phe	Asp	Ala	Ser	Arg	Gln	Ser	Met	Gly	Ala	Gly	Ser	His	Ser	Leu
	595						600					605			
Thr	Tyr	Glu	Leu	Thr	Pro	Ala	Gly	Leu	Gln	Val	Lys	Ile	Ser	Ser	Asn
	610					615					620				
Gly	Leu	Asp	Cys	Thr	Ala	Thr	Phe	Pro	Xaa	Gly	Gly	Ala	Pro	Ser	Ala
625					630					635					640
Ala	Pro	Gly	Glu	Val	Xaa	Ala	Phe	Cys	Ser	Ala	Leu	Tyr	Arg	Tyr	Asn
			645					650						655	
Arg	Phe	Thr	Gln	Arg	His	Ser	Leu	Thr	Gly	Gly	Leu	Trp	Leu	His	Pro
			660					665					670		
Glu	Gly	Leu	Leu	Gly	Ile	Phe	Pro	Pro	Phe	Ser	Pro	Gly	His	Ile	Trp
	675					680						685			
Glu	Ser	Ala	Asn	Pro	Phe	Cys	Gly	Glu	Gly	Thr	Leu	Tyr	Thr	Arg	Thr
	690					695					700				
Trp	Ser	Thr	Ser	Gly	Phe	Ser	Ser	Asp	Phe	Ser	Pro	Pro	Glu	Ala	Ala
705					710					715					720
Ala	Pro	Ala	Ser	Ala	Ala	Ala	Pro	Gly	Leu	Pro	Tyr	Pro	Thr	Pro	Pro

				725					730					735			
Val	Ser	Asp	Ile	Trp	Val	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Ser	His	Val		
			740					745					750				
Asp	Ala	Ala	Ser	Val	Pro	Ser	Val	Pro	Glu	Pro	Ala	Gly	Leu	Thr	Ser		
		755					760					765					
Pro	Ile	Val	Leu	Thr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val	Arg	Lys	Pro		
	770					775					780						
Ala	Thr	Ser	Pro	Pro	Pro	Arg	Thr	Arg	Arg	Leu	Leu	Tyr	Thr	Tyr	Pro		
785					790					795					800		
Asp	Gly	Ala	Lys	Val	Tyr	Ala	Gly	Ser	Leu	Xaa	Glu	Ser	Asp	Cys	Asp		
			805					810						815			
Trp	Leu	Val	Asn	Ala	Ser	Asn	Pro	Gly	His	Arg	Pro	Gly	Gly	Gly	Leu		
		820						825					830				
Cys	His	Ala	Phe	Tyr	Gln	Arg	Phe	Pro	Glu	Ala	Phe	Tyr	Ser	Thr	Glu		
		835					840					845					
Phe	Ile	Met	Arg	Glu	Gly	Leu	Ala	Ala	Tyr	Thr	Leu	Thr	Pro	Arg	Pro		
	850					855					860						
Ile	Ile	His	Ala	Val	Ala	Pro	Asp	Tyr	Arg	Val	Glu	Gln	Asn	Pro	Lys		
865					870					875					880		
Arg	Leu	Glu	Ala	Ala	Tyr	Arg	Glu	Thr	Cys	Ser	Arg	Arg	Gly	Thr	Ala		
			885					890						895			
Ala	Tyr	Pro	Leu	Leu	Gly	Ser	Gly	Ile	Tyr	Gln	Val	Pro	Val	Ser	Leu		
		900					905						910				
Ser	Phe	Asp	Ala	Trp	Glu	Arg	Asn	His	Arg	Pro	Gly	Asp	Glu	Leu	Tyr		
		915					920					925					
Leu	Thr	Glu	Pro	Ala	Ala	Ala	Trp	Phe	Glu	Ala	Asn	Lys	Pro	Ala	Gln		
	930					935					940						
Pro	Ala	Leu	Thr	Ile	Thr	Glu	Asp	Thr	Ala	Arg	Thr	Ala	Asn	Leu	Ala		
945					950					955					960		
Leu	Glu	Ile	Asp	Ala	Ala	Thr	Glu	Val	Gly	Arg	Ala	Cys	Ala	Gly	Cys		
			965					970						975			
Thr	Ile	Ser	Pro	Gly	Ile	Val	His	Tyr	Gln	Phe	Thr	Ala	Gly	Val	Pro		
		980					985						990				
Gly	Ser	Gly	Lys	Ser	Arg	Ser	Ile	Gln	Gln	Gly	Asp	Val	Asp	Val	Val		
	995						1000					1005					
Val	Val	Pro	Thr	Arg	Glu	Leu	Arg	Asn	Ser	Trp	Arg	Arg	Arg	Gly	Phe		
	1010					1015					1020						
Ala	Ala	Phe	Thr	Pro	His	Thr	Ala	Ala	Arg	Val	Thr	Ile	Gly	Arg	Arg		
1025					1030					1035					1040		
Val	Val	Ile	Asp	Glu	Ala	Pro	Ser	Leu	Pro	Pro	His	Leu	Leu	Leu	Leu		
			1045						1050					1055			
His	Met	Gln	Arg	Ala	Ser	Ser	Val	His	Leu	Leu	Gly	Asp	Pro	Asn	Gln		
		1060						1065					1070				
Ile	Pro	Ala	Ile	Asp	Phe	Glu	His	Ala	Gly	Leu	Val	Pro	Ala	Ile	Arg		
		1075					1080					1085					
Pro	Glu	Leu	Ala	Pro	Thr	Ser	Trp	Trp	His	Val	Thr	His	Arg	Cys	Pro		
	1090					1095					1100						
Ala	Asp	Val	Cys	Glu	Leu	Ile	Arg	Gly	Ala	Tyr	Pro	Lys	Ile	Gln	Thr		
1105					1110					1115					1120		
Thr	Ser	Arg	Val	Leu	Arg	Ser	Leu	Phe	Trp	Asn	Glu	Pro	Ala	Ile	Gly		
			1125						1130					1135			
Gln	Lys	Leu	Val	Phe	Thr	Gln	Ala	Ala	Lys	Ala	Ala	Asn	Pro	Gly	Ala		
		1140						1145					1150				
Ile	Thr	Val	His	Glu	Ala	Gln	Gly	Ala	Thr	Phe	Thr	Glu	Thr	Thr	Ile		
		1155					1160					1165					
Ile	Ala	Thr	Ala	Asp	Ala	Arg	Gly	Leu	Ile	Gln	Ser	Ser	Arg	Ala	His		
	1170					1175						1180					

Ala Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Leu Asp
 1185 1190 1195 1200
 Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Val Ile Val Asn
 1205 1210 1215
 Asn Phe Phe Leu Ala Gly Gly Glu Val Gly His His Arg Pro Ser Val
 1220 1225 1230
 Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu Gly Thr Leu Gln Ala Phe
 1235 1240 1245
 Pro Pro Ser Cys Gln Ile Ser Ala Tyr His Gln Leu Ala Glu Glu Leu
 1250 1255 1260
 Gly His Arg Pro Ala Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu
 1265 1270 1275 1280
 Leu Glu Gln Gly Leu Leu Tyr Met Pro Gln Glu Leu Thr Val Ser Asp
 1285 1290 1295
 Ser Val Leu Val Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala
 1300 1305 1310
 Ala Pro Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr
 1315 1320 1325
 Gly Arg Arg Thr Lys Leu Tyr Glu Ala Ala His Ser Asp Val Arg Glu
 1330 1335 1340
 Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly Pro Val Arg Ala Thr Thr
 1345 1350 1355 1360
 Cys Glu Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp
 1365 1370 1375
 Gly Ser Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg
 1380 1385 1390
 Ile Thr Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr
 1395 1400 1405
 Ile Ala His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr
 1410 1415 1420
 Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Glu Ile
 1425 1430 1435 1440
 Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr Gly Asp Ala Tyr Glu Glu
 1445 1450 1455
 Ser Val Phe Ala Ala Ala Val Ser Gly Ala Gly Ser Cys Met Val Phe
 1460 1465 1470
 Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu
 1475 1480 1485
 Gly Leu Glu Cys Val Val Met Glu Glu Cys Gly Met Pro Gln Trp Leu
 1490 1495 1500
 Ile Arg Leu Tyr His Leu Val Arg Ser Ala Trp Ile Leu Gln Ala Pro
 1505 1510 1515 1520
 Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly
 1525 1530 1535
 Thr Leu Leu Trp Asn Thr Val Trp Asn Met Ala Ile Ile Ala His Cys
 1540 1545 1550
 Xaa Glu Phe Arg Asp Phe Arg Val Ala Ala Phe Lys Gly Asp Asp Ser
 1555 1560 1565
 Val Val Leu Cys Ser Asp Tyr Arg Gln Xaa Arg Asn Ala Ala Ala Leu
 1570 1575 1580
 Ile Ala Gly Cys Gly Leu Lys Leu Lys Val Asp Tyr Arg Pro Ile Gly
 1585 1590 1595 1600
 Leu Tyr Ala Gly Val Val Val Ala Pro Gly Leu Gly Thr Leu Pro Asp
 1605 1610 1615
 Val Val Arg Phe Ala Gly Arg Leu Ser Glu Lys Asn Trp Gly Pro Gly
 1620 1625 1630
 Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala Val Cys Asp Phe Leu Arg

	1635		1640		1645										
Gly	Leu	Thr	Asn	Val	Ala	Gln	Val	Cys	Val	Asp	Val	Val	Ser	Arg	Val
	1650					1655				1660					
Tyr	Gly	Val	Ser	Pro	Gly	Leu	Val	His	Asn	Leu	Ile	Gly	Met	Leu	Gln
1665					1670					1675				1680	
Thr	Ile	Ala	Asp	Gly	Lys	Ala	His	Phe	Thr	Xaa	Asn	Ile	Lys	Pro	Val
			1685					1690					1695		
Leu	Asp	Leu	Thr	Asn	Ser	Ile	Ile	Gln	Arg	Val	Glu				
		1700						1705							

<210> 167
 <211> 660
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 84
 <223> Xaa = Unknown or Other at position 230
 <223> Xaa = Unknown or Other at position 447

<400> 167

Met	Arg	Pro	Arg	Ala	Val	Leu	Leu	Leu	Leu	Phe	Val	Leu	Leu	Pro	Met
1				5					10					15	
Leu	Pro	Ala	Pro	Pro	Ala	Gly	Gln	Pro	Ser	Gly	Arg	Arg	Arg	Gly	Arg
			20					25					30		
Arg	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Phe	Trp	Gly	Asp	Arg	Val	Asp	Ser
		35				40					45				
Gln	Pro	Phe	Ala	Leu	Pro	Tyr	Ile	His	Pro	Thr	Asn	Pro	Phe	Ala	Ala
	50					55					60				
Asp	Val	Val	Ser	Gln	Pro	Gly	Ala	Gly	Thr	Arg	Pro	Arg	Gln	Pro	Pro
65				70					75					80	
Arg	Pro	Leu	Xaa	Ser	Ala	Trp	Arg	Asp	Gln	Ser	Gln	Arg	Pro	Ser	Ala
			85					90						95	
Ala	Pro	Arg	Arg	Arg	Ser	Ala	Pro	Ala	Gly	Ala	Ala	Pro	Leu	Thr	Ala
			100					105					110		
Val	Ser	Pro	Ala	Pro	Asp	Thr	Ala	Pro	Val	Pro	Asp	Val	Asp	Ser	Arg
		115				120					125				
Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	Thr
	130					135					140				
Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	Leu
145				150					155					160	
Asn	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	Ala
			165					170						175	
Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Val	Arg	Ala	Thr	Ile
			180					185					190		
Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	Ser
	195					200						205			
Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	Met
	210					215					220				
Asn	Ser	Ile	Thr	Ser	Xaa	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	Ile
225				230						235				240	
Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	Gln
			245					250						255	
Gly	Trp	Arg	Ser	Val	Glu	Thr	Thr	Gly	Val	Ala	Glu	Glu	Glu	Ala	Thr
			260					265						270	

Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	Tyr
		275					280					285			
Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	Leu
		290				295					300				
Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	Val
305					310					315					320
Ser	Arg	Tyr	Thr	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	Asp
				325					330					335	
Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp
			340					345					350		
Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile
		355					360					365			
Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro
		370				375					380				
Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro
385					390					395					400
Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
				405					410					415	
Glu	Asn	Ala	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	
			420				425						430		
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	Xaa	Glu
		435					440					445			
Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val
		450				455					460				
Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr
465					470					475					480
Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr	Val	Ser	Asp
				485					490					495	
Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg
			500					505					510		
Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Thr	Thr
		515					520					525			
Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val	Leu	Pro	Leu	Arg	Gly	Lys
	530					535					540				
Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn
545					550					555					560
Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala	Gly
				565					570					575	
His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly	Pro
			580					585					590		
Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala	Pro	His	Ser	Ala	Leu	Ala
		595				600						605			
Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp
	610					615				620					
Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe
625					630					635					640
Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys	Val	Gly	Lys
				645					650					655	
Thr	Arg	Glu	Ser												
			660												

<210> 168

<211> 122

<212> PRT

<213> Hepatitis E Virus

<220>

77/117

<223> us2 orf3

<223> Xaa = Unknown or Other at position 97

<400> 168

Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys	Ala	Leu
1				5					10					15	
Gly	Leu	Phe	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys	Pro	Arg	
			20				25					30			
His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Ala	Ala	Ala
		35				40					45				
Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser	Pro	Ser
	50				55				60						
Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met	Ser	Phe
65				70					75					80	
His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala	Pro	Leu
			85					90						95	
Xaa	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro	Pro	Val
		100					105					110			
Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg						
	115						120								

<210> 169

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 4-2

<400> 169

Ala	Asn	Gln	Pro	Gly	His	Leu	Ala	Pro	Leu	Gly	Glu	Ile	Arg	Pro	Ser
1				5				10						15	
Ala	Pro	Pro	Leu	Pro	Pro	Val	Ala	Asp	Leu	Pro	Gln	Pro	Gly	Leu	Arg
			20					25					30		

Arg

<210> 170

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> M 3-2e

<400> 170

Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5				10						15	
Glu	Cys	Arg	Ala	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20				25					30			
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Val	Lys	Val	Gly	Lys	Thr	Arg	Glu	Leu
	35					40						45			

<210> 171

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> B 4-2

<400> 171

Ala	Asn	Pro	Pro	Asp	His	Ser	Ala	Pro	Leu	Gly	Val	Thr	Arg	Pro	Ser
1				5					10					15	
Ala	Pro	Pro	Leu	Pro	His	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Pro	Arg
			20					25					30		

Arg

<210> 172

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> B 3-2e

<400> 172

Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	
Glu	Cys	Arg	Pro	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20					25					30		
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Leu
		35					40					45			

<210> 173

<211> 33

<212> PRT

<213> Hepatitis E Virus

<220>

<223> OFR3 (u4.2)

<400> 173

Asp	Ser	Arg	Pro	Ala	Pro	Ser	Val	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser
1				5					10					15	
Ala	Pro	Pro	Leu	Pro	Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg
			20					25					30		

Arg

<210> 174

<211> 48

<212> PRT

<213> Hepatitis E Virus

<220>

<223> ORF2 (u3.2e)

<400> 174

Thr	Val	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	
Glu	Cys	Arg	Thr	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile

79/117

Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser

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<210> 175
<211> 327
<212> PRT
<213> Hepatitis E Virus
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<220>
<223> US-1 SG3

<223> Xaa = Unknown or Other at position 148

<223> Xaa = Unknown or Other at position 209

<223> Xaa = Unknown or Other at position 262

175															
Gly 1	Ala	Asp	Gly	Thr 5	Ala	Glu	Leu	Thr	Thr 10	Thr	Ala	Ala	Thr 15	Arg	Phe
Met	Lys	Asp	Leu 20	His	Phe	Thr	Gly	Thr 25	Asn	Gly	Val	Gly	Glu 30	Val	Gly
Arg	Gly	Ile 35	Ala	Leu	Thr	Leu	Phe 40	Asn	Leu	Ala	Asp 45	Thr	Leu	Leu	Gly
Gly	Leu 50	Pro	Thr	Glu	Leu	Ile 55	Ser	Ser	Ala	Gly	Gly 60	Gln	Leu	Phe	Tyr
Ser 65	Arg	Pro	Val	Val	Ser 70	Ala	Asn	Gly	Glu	Pro	Thr 75	Val	Lys	Leu	Tyr 80
Thr	Ser	Val	Glu	Asn 85	Ala	Gln	Gln	Asp	Lys 90	Gly	Ile	Thr	Ile	Pro 95	His
Asp	Ile	Asp	Leu 100	Gly	Asp	Ser	Arg	Val 105	Val	Ile	Gln	Asp	Tyr 110	Asp	Asn
Gln	His	Glu	Gln 115	Asp	Arg	Pro	Thr 120	Pro	Ser	Pro	Ala	Pro 125	Ser	Arg	Pro
Phe	Ser	Val	Leu	Arg	Ala	Asn 135	Asp	Val	Leu	Trp	Leu 140	Ser	Leu	Thr	Ala
Ala 145	Glu	Tyr	Xaa	Gln	Thr 150	Thr	Tyr	Gly	Ser	Ser 155	Thr	Asn	Pro	Met	Tyr 160
Val	Ser	Asp	Thr	Val 165	Thr	Leu	Val	Asn	Val 170	Ala	Thr	Gly	Ala	Gln	Ala 175
Val	Ala	Arg	Ser 180	Leu	Asp	Trp	Ser	Lys 185	Val	Val	Thr	Leu	Asp 190	Gly	Arg
Leu	Thr	Thr 195	Ile	Gln	Gln	Tyr	Ser 200	Lys	Lys	Phe	Tyr	Val 205	Leu	Pro	Leu
Xaa 210	Gly	Lys	Leu	Ser	Phe	Trp 215	Glu	Ala	Gly	Thr	Thr 220	Lys	Ala	Gly	Tyr
Pro 225	Tyr	Asn	Tyr	Asn 230	Thr	Ala	Ser	Asp	Gln 235	Ile	Leu	Ile	Glu	Asn 240	
Ala	Ala	Gly	His 245	Arg	Val	Ala	Ile	Ser	Thr 250	Tyr	Thr	Thr	Ser	Leu	Gly 255
Ala	Gly	Pro	Thr 260	Ser	Xaa	Ser	Ala	Val 265	Gly	Val	Leu	Ala	Pro	His	Ser
Ala	Leu	Ala 275	Val	Leu	Glu	Asp	Thr 280	Val	Asp	Tyr	Pro	Ala	Arg	Ala	His
Thr	Phe 290	Asp	Asp	Phe	Cys	Pro 295	Glu	Cys	Arg	Thr	Leu 300	Gly	Leu	Gln	Gly

80/117

Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys
 305 310 315 320
 Val Gly Lys Thr Arg Glu Ser
 325

<210> 176
 <211> 327
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> US-2 SG3

<223> Xaa = Unknown or Other at position 114

<400> 176
 Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe
 1 5 10 15
 Met Lys Asp Leu His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly
 20 25 30
 Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly
 35 40 45
 Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr
 50 55 60
 Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr
 65 70 75 80
 Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His
 85 90 95
 Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn
 100 105 110
 Gln Xaa Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro
 115 120 125
 Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala
 130 135 140
 Ala Glu Tyr Asp Gln Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr
 145 150 155 160
 Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala
 165 170 175
 Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro
 180 185 190
 Leu Thr Thr Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu
 195 200 205
 Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr
 210 215 220
 Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn
 225 230 235 240
 Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly
 245 250 255
 Ala Gly Pro Thr Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser
 260 265 270
 Ala Leu Ala Val Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His
 275 280 285
 Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly
 290 295 300
 Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys
 305 310 315 320
 Val Gly Lys Thr Arg Glu Ser

325

<210> 177
 <211> 21
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> HEVConsORF1-s2

 <400> 177
 ctgcccytkgc gaatgctgtg g 21

 <210> 178
 <211> 24
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> HEVConsORF1-a2

 <400> 178
 ggcagwrtac carcgtgaa catc 24

 <210> 179
 <211> 294
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> z12-orf1 (G.S.)

 <400> 179
 tggcattact actgccattg agcaagctgc tctggctgcg gcccaattctg ccttggcgaa 60
 tgctgtggtg gttcggccgt ttttatctcg tttacagact gagattctta ttaatttgat 120
 gcaaccccg cagttggtct ttcgacctga ggtgttctgg aaccatccca tccaacgtgt 180
 tatacataat gaattggagc agtactgccg ggcccgggcc ggtcgctgtc tggaaattgg 240
 agcccatcca aggtcaatca atgataatcc taatgttctg catcggtgtt tcct 294

 <210> 180
 <211> 418
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> z12-orf1.con

 <400> 180
 ctggcattac tactgctatt gagcaagctg ctctgggtgc ggccaattct gccttggcga 60
 atgctgtggt ggttcggccg ttttatctcg gtttacagac tgagattctt attaatttga 120
 tgcaaccccg acagttggtc tttcgacctg aggtgttctg gaaccatccc atccaacgtg 180
 ttatacataa tgaattggag cagtactgcc gggcccgggc cggtcgctgt ctggaaattg 240
 gagcccatcc aaggtcaatc aatgataatc ctaatgttct gcacgggtgc tttttacgac 300
 cggtcgggag ggaogttcag cgctgggtact ccgccccac ccgtggcccc gcggccaact 360
 gccgcgggtc tgcgctgcgt ggtctcccc ctgtcgaccg cacttactgc ctcgatgg 418

 <210> 181

<211> 197
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> z12-orf2.con

 <400> 181
 gacagaatta atttcgctcg ctgggggtca actgttctac tcccgcctg tcgtctcagc 60
 caatggcgag ccgactgtca agttatacac atctgttgag aatgcacagc aggataaggg 120
 gatagctatt ccacatgaca tagatttggg cgactctcgt ttggtaatcc aggattatga 180
 taaccaacac gaacaag 197

 <210> 182
 <211> 25
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> HEVConsORF2/3-s1

 <400> 182
 gtatcggkyk gaatgaataa catgt 25

 <210> 183
 <211> 25
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> HEVConsORF2/3-a1

 <400> 183
 aggggttggt tggatgaata taggg 25

 <210> 184
 <211> 234
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> z12.orf23.con

 <400> 184
 gtatcggktt gaatgaataa catgttttgt gcatcgccca tgggatcacc atgcgccta 60
 gggttgttct gttgttgttc ctctgttttc tgcctatgct gcccgcgcca ccggccggcc 120
 agycgactgg ccgccgtcgt gggcgcgca gcggcggtgc cggcggtggt ttctgggggtg 180
 acagggttga ttctcagccc ttccgacctc cctatatcca tccaaccaac ccct 234

 <210> 185
 <211> 890
 <212> DNA
 <213> Hepatitis E Virus

 <220>
 <223> z12-3p.race

<400> 185

gtcgtctcgg	ccaatggcga	gccgactgtc	aagttataca	catctgttga	gaatgcacag	60
caggataagg	ggatagctat	tccacatgac	atagatttgg	gcgactctcg	tttggtaatc	120
caggattacg	ataatcagca	cgagcaggac	cggcccaccc	cttcgcccgc	cccgtctcgt	180
cctttctcgg	tcctccgcgc	taatgatgct	ttgtggcttt	ctcttaccgc	tgctgagtat	240
gaccagacta	catatgggtc	gtccaccaac	ccgatgtatg	tctcagacac	tgftacattt	300
gtcaatgtgg	ccacaggggc	tcaggctgtc	gcccgtttct	ttgattgggc	taaagttacc	360
ctggacggcc	gccctcttac	taccatccag	cagtactcta	agacatttta	tgttctccca	420
cttcgcggga	agttatcttt	ttgggaggct	ggcacaacta	aagccgggta	cccttataat	480
tataacacaa	ctgctagtga	ccagattctg	attgaaaacg	cggctggcca	tcgtgtcgc	540
atatctactt	atactactag	cctgggcgcc	ggccctgtgt	cagtttctgc	ggttgggtgtg	600
ttagccccac	actcgagcct	tgctattctt	gaagacactg	ttgactatcc	ggcccgtgct	660
cacacttttg	atgacttctg	tccggaatgc	cgtgccctgg	gtctgcaggg	gtgtgctttt	720
caatctacta	tcgctgagct	ccagcgtctt	aaaatgaagg	taggcaaaac	ccgggagttt	780
taattaattc	ttcttgtgcc	cccttcacgg	ttctcgcttt	atttctttct	tctgcctccc	840
gcgctccctg	gaaaaaaaaa	aaaaaaaaaa	gtactagtgc	acgcgtggcc		890

<210> 186

<211> 919

<212> DNA

<213> Hepatitis E Virus

<220>

<223> z12-3p.con

<400> 186

gacagaatta	atttcgtcgg	ctgggggtca	actgtttctac	tcccgcctcg	tcgtctcagc	60
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gatagctatt	ccacatgaca	tagatttggg	cgactctcgt	ttggtaatcc	aggattacga	180
taatcagcac	gagcaggacc	ggcccacccc	ttcgcccgc	ccgtctcgtc	ctttctcggg	240
cctccgcgct	aatgatgctt	tgtggctttc	tcttaccgct	gctgagtatg	accagactac	300
atatgggtcg	tccaccaacc	cgatgtatgt	ctcagacact	gttacatttg	tcaatgtggc	360
cacaggggct	caggctgtcg	cccgttctct	tgattgggtc	aaagttaccc	tggaacggccg	420
ccctcttact	accatccagc	agtactctaa	gacattttat	gtttctccac	ttcgcgggaa	480
gttatctttt	tgggaggctg	gcacaactaa	agccggttac	ccttataatt	ataacacaac	540
tgctagtgc	cagattctga	ttgaaaacgc	ggctggccat	cgtgtcgcta	tatctactta	600
tactactagc	ctgggcgcgc	gccctgtgtc	agtttctgcg	gttggtgtgt	tagccccaca	660
ctcgagcctt	gctattcttg	aagacactgt	tgactatccg	gcccgtgctc	acacttttga	720
tgacttctgt	ccggaatgcc	gtgccctggg	tctgcagggg	tgtgcttttc	aatctactat	780
cgctgagctc	cagcgtctta	aatgaagg	aggcaaaacc	cgggagtttt	aattaattct	840
tcttgtgccc	ccttcacggg	tctcgcttta	tttctttctt	ctgcctcccc	cgctccctgg	900
aaaaaaaaaa	aaaaaaaaaa					919

<210> 187

<211> 138

<212> PRT

<213> Hepatitis E Virus

<220>

<223> z12-orf1.pep

<400> 187

Gly	Ile	Thr	Thr	Ala	Ile	Glu	Gln	Ala	Ala	Leu	Gly	Ala	Ala	Asn	Ser
1			5					10						15	
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Leu	Gln
			20					25						30	
Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg

35							40					45				
Pro	Glu	Val	Phe	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	
50						55	60									
Leu	Glu	Gln	Tyr	Cys	Arg	Ala	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Ile	Gly	
65					70		75					80				
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Leu	His	Arg	Cys	
85				90					95							
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro	
100			105					110								
Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu	
115		120					125									
Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Leu	Asp							
130						135										

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<210> 188
<211> 61
<212> PRT
<213> Hepatitis E Virus
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<220>
<223> z12-orf2-5'.pep

<223> Xaa = Unknown or Other at position 25

<400> 188															
Met	Arg	Pro	Arg	Val	Val	Leu	Leu	Leu	Phe	Leu	Val	Phe	Leu	Pro	Met
1				5					10					15	
Leu	Pro	Ala	Pro	Pro	Ala	Gly	Gln	Xaa	Thr	Gly	Arg	Arg	Arg	Gly	Arg
			20					25					30		
Arg	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Phe	Trp	Gly	Asp	Arg	Val	Asp	Ser
		35					40					45			
Gln	Pro	Phe	Ala	Leu	Pro	Tyr	Ile	His	Pro	Thr	Asn	Pro			
	50					55					60				

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<210> 189
<211> 276
<212> PRT
<213> Hepatitis E Virus
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<220>
<223> z12-orf2-3'.pep

	<400> 189														
Thr 1	Glu	Leu	Ile	Ser 5	Ser	Ala	Gly	Gly	Gln 10	Leu	Phe	Tyr	Ser 15	Arg	Pro
Val	Val	Ser	Ala 20	Asn	Gly	Glu	Pro	Thr 25	Val	Lys	Leu	Tyr	Thr 30	Ser	Val
Glu	Asn	Ala 35	Gln	Gln	Asp	Lys	Gly 40	Ile	Ala	Ile	Pro	His 45	Asp	Ile	Asp
Leu	Gly 50	Asp	Ser	Arg	Leu	Val 55	Ile	Gln	Asp	Tyr	Asp 60	Asn	Gln	His	Glu
Gln 65	Asp	Arg	Pro	Thr 70	Pro	Ser	Pro	Ala	Pro	Ser 75	Arg	Pro	Phe	Ser 80	Val
Leu	Arg	Ala	Asn 85	Asp	Ala	Leu	Trp	Leu	Ser 90	Leu	Thr	Ala	Ala 95	Glu	Tyr
Asp	Gln	Thr	Thr 100	Tyr	Gly	Ser	Ser	Thr 105	Asn	Pro	Met	Tyr	Val 110	Ser	Asp

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Thr Val Thr Phe Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg
      115                      120                      125
Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr
      130                      135                      140
Ile Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys
145                      150                      155                      160
Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
      165                      170                      175
Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly
      180                      185                      190
His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
      195                      200                      205
Val Ser Val Ser Ala Val Gly Val Leu Ala Pro His Ser Ser Leu Ala
      210                      215                      220
Ile Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
225                      230                      235                      240
Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe
      245                      250                      255
Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
      260                      265                      270
Thr Arg Glu Phe
      275

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<210> 190
<211> 74
<212> PRT
<213> Hepatitis E Virus

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```

<220>
<223> z12-orf3.pep

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<400> 190
Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
 1      5      10      15
Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
      20      25      30
His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
      35      40      45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
      50      55      60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
65                      70

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<210> 191
<211> 408
<212> DNA
<213> Hepatitis E Virus

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```

<220>
<223> pJOorf3-29.seq

```

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<400> 191
gaattcatga ataacatgtc ttttgcacgc cccatgggat caccatgcgc cctagggctg      60
ttctgttgtt gctcttcgtg cttttgccta tgctgccgcg gccaccggcc agccagccgt      120
ctggccgcgc tcgtggggcg cgcagcggcg gtgccggcgg tggtttctgg ggtgacaggg      180
ttgattctca gcccttcgcc ctcccctata ttcacccaac caacccttc gccgccgatg      240
tcgtttcaca acccgggggt ggaactcgcc ctgcacagcc gccccgcccc cttggctccg      300

```

cttggcggtga	ccagtgcccag	cgccccctccg	ctgcccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	gcgactacaa	ggacgacgat	gacaagtaat	aaggatcc		408

<210> 192
 <211> 1026
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> cksorf2m-2.seq

<400> 192						
gaattcatgg	gtgctgatgg	gactgctgag	cttactacca	cagcagccac	acgtttcatg	60
aaggacctgc	acttcgctgg	cacgaatggc	gttgggtgagg	tgggtcgtgg	tatcgccctg	120
acactgttca	atctcgctga	tacgcttctc	ggcgggtttac	cgacagaatt	gatttcgctg	180
gctggggggc	aactgtttta	ctcccgcccg	gttgtctcag	ccaatggcga	gccaacagta	240
aagttatata	catctgttga	gaatgcgcag	caagacaagg	gcataccat	tccacatgat	300
atagacctgg	gtgactcccg	tgtggttate	caggattatg	ataaccagca	tgagcaagac	360
cgacctactc	cgtcacctgc	cccctctcgc	cccttctcag	ttcttcgtgc	caatgatgtt	420
ttgtggcttt	ccctcactgc	cgctgagtat	gaccagacta	cgtatgggtc	gtccaccaac	480
cctatgtatg	tctctgacac	agttacgctt	gttaatgtgg	ctactgggtc	tcaggctgtt	540
gcccgtctcc	ttgattggtc	taaagttact	ctggacggcc	gcccccttac	taccattcag	600
cagtattcta	agacatttta	tgttctcccg	ctccgcggga	agctgtcctt	ttgggaggct	660
ggcacgacta	aggccggcta	cccttacaat	tataatacta	ccgctagtga	ccaaattttg	720
attgagaatg	cggcgggcca	ccgtgtcgct	atttccacct	ataccactag	cttaggtgcc	780
ggtcctacct	cgatctctgc	ggtcggcgta	ctggctccac	actctgccct	tgccgttctt	840
gaggatacta	ttgattaccc	cgcccgtgcc	catacttttg	atgatttttg	cccggagtgc	900
cgtaccctag	gtttgagggg	ttgtgcattc	cagtcacta	ttgctgagct	ccagcgttta	960
aaaatgaagg	taggtaaaac	ccgggagctc	gactacaagg	acgacgatga	caagtaataa	1020
ggatcc						1026

<210> 193
 <211> 1389
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> CKSORF32M-3.seq

<400> 193						
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ctggccgcgc	tcgtagggcg	cgtagcggcg	gtgccggcg	tggtttctgg	ggtgacaggg	180
ttgattctca	gcccttcgcc	ctccccata	ttcatccaac	caacccttc	gccgccgatg	240
tcgtttcaca	accgggggct	ggaactcgcc	ctcgacagcc	gccccgccc	cttggctccg	300
cttggcgtga	ccagtgcccag	cgccctcccg	ctgccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	ggggtgctga	tgggactgct	gagcttacta	ccacagcagc	cacacgtttc	420
atgaaggacc	tgcacttcgc	tggcacgaat	ggcgttggtg	aggtgggtcg	tggtatcgcc	480
ctgacactgt	tcaatctcgc	tgatacgtt	ctcgccgggt	taccgacaga	attgatttcg	540
tcggctgggg	gccaactgtt	ttactccgc	ccggttgtct	cagccaatgg	cgagccaaca	600
gtaaagttat	atacatctgt	tgagaatgcg	cagcaagaca	agggcatcac	cattccacat	660
gatatagacc	tgggtgactc	ccgtgtgggt	atccaggatt	atgataacca	gcatagcaa	720
gaccgaccta	ctcgcgcacc	tgccccctct	cgccccctct	cagttcttcg	tgccaatgat	780
gttttgtggc	tttccctcac	tgccgctgag	tatgaccaga	ctacgtatgg	gtcgtccacc	840
aaccctatgt	atgtctctga	cacagttacg	cttgttaatg	tggctactgg	tgctcaggct	900
gttgcccgtc	cccttgattg	gtctaaagtt	actctggacg	gcccggccct	tactaccatt	960
cagcagtatt	ctaagacatt	ttatgtttct	ccgctccgcg	ggaagctgtc	cttttggggg	1020

gctggcacga	ctaaggccgg	ctacccttac	aattataata	ctaccgctag	tgaccaaatt	1080
ttgattgaga	atgcggccgg	ccaccgtgtc	gctatttcca	cctataccac	tagcttaggt	1140
gccggtccta	cctcgatctc	tgcggtcggc	gtactggctc	cacactctgc	ccttgccgtt	1200
cttgaggata	ctattgatta	ccccgcccg	gcccatactt	ttgatgattt	ttgcccgagg	1260
tgccgtaccc	taggtttgca	gggttgtgca	ttccagtcta	ctattgctga	gctccagcgt	1320
ttaaaaatga	aggtaggtaa	aaccgcggag	tctgactaca	aggacgacga	tgacaagtaa	1380
taaggatcc						1389

<210> 194
 <211> 408
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> plorf3-12.con

<400> 194						
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ttctgttggt	gctcttcgtg	cttttgcccta	tgctgcccgc	gccaccggcc	ggccagccgt	120
ctggccgcgg	tcgtggggcg	cgccagcgcg	gtgccggcg	tggtttctgg	ggtgacagg	180
ttgattctca	gcccttcgcc	ctcccctata	ttcatccaac	caacccttc	gccgccgatg	240
tcgtttcaca	acccggggct	ggaactcgcc	ctcgacagcc	gccccgcccc	cttggtctcg	300
cttggcgtga	ccagtcccag	cgcccctccg	ctgccccccg	tcgtcgatct	gccccagctt	360
ggtctgcgcc	gcgactacaa	ggacgacgat	gacaagtaat	aaggatcc		408

<210> 195
 <211> 1026
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> plorf2.2-6.seq

<400> 195						
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acactgttca	atctcgctga	tacgcttctc	ggcggtttac	cgacagaatt	gatttcgtcg	180
gctggggggc	aactgtttta	ctcccgcccc	gttgtctcag	ccaatggcga	gccaacagta	240
aagttatata	catctgttga	gaatgcgcag	caagacaagg	gcacacccat	tccacatgat	300
atagacctgg	gtgactcccg	tgtggttatc	caggattatg	ataaccagca	tgagcaagac	360
cgacctactc	cgtcacctgc	cccctctcgc	cccttctcag	ttcttcgtgc	caatgatgtt	420
ttgtggcttt	ccctcactgc	cgctgagtat	gaccagacta	cgtatgggtc	gtccaccaac	480
cctatgtatg	tctctgacac	agttacgctt	gttaatgtgg	ctactgggtc	tcaggctgtt	540
gcccgtctcc	ttgattgggtc	taaagttact	ctggacggcc	gcccccttac	taccattcag	600
cagtattcta	agacatttta	tgttctcccc	ctccgcggga	agctgtcctt	ttgggaggct	660
ggcacgacta	aggccgggcta	cccttacaat	tataatacta	ccgctagtga	ccaaattttg	720
attgagaatg	cggccggcca	ccgtgtcgct	atttccacct	ataccactag	cttaggtgcc	780
ggtcctacct	cgatctctgc	ggtcggcgta	ctggctccac	actctgccct	tgccgttctt	840
gaggatacta	ttgattaccc	cgcccgtgcc	catacttttg	atgatttttg	cccggagtgc	900
cgtaccctag	gtttgcagg	ttgtgcattc	cagtctacta	ttgtgagct	ccagcgttta	960
aaaatgaagg	taggtaaaac	ccgggagctc	gactacaagg	acgacgatga	caagtaataa	1020
g gatcc						1026

<210> 196
 <211> 1389
 <212> DNA
 <213> Hepatitis E Virus

<220>

<223> PLORF32M-14-5.seq

<400> 196

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ttctgttggt gctcttcgtg cttttgccta tgctgcccgc gccaccggcc agccagccgt      120
ctggccgccg tcgtggggcg cgtagcggcg gtgccggcgg tggtttctgg ggtgacaggg      180
ttgattctca gcccttcgcc ctcccctata ttcattccaa caacccttc gccgccgatg      240
tcgtttcaca acccgggggt ggaactcgcc ctcgacagcc gccccgcccc cttggctccg      300
cttggcgtga ccagtcccag cgccccctcg ctgccccccg tcgtcgatct gcccagctt      360
ggtctgcgcc gcggtgctga tgggactgct gagcttacta ccacagcagc cacacgtttc      420
atgaaggacc tgcacttcgc tggcacgaat ggcgttggtg aggtgggtcg tggtatcgcc      480
ctgacactgt tcaatctcgc tgatacgctt ctcggcgggt taccgacaga attgatttcg      540
tcggctgggg gccaaactgt ttactccgcg ccggttggtc cagccaatgg cgagccaaca      600
gtaaagttat atacatctgt tgagaatgcg cagcaagaca agggcatcac cattccacat      660
gatatagacc tgggtgactc ccgtgtggtt atccaggatt atgataacca gcatgagcaa      720
gaccgacctt ctcgcgcacc tgccccctct cgccccctct cagttcttcg tgccaatgat      780
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aaccctatgt atgtctctga cacagttacg cttgttaatg tggtactagg tgctcaggct      900
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cagcagtatt ctaagacatt ttatgttctc ccgctccgcg ggaagctgtc cttttgggag     1020
gctggcacga ctaaggccgg ctacccttac aattataata ctaccgctag tgaccaaatt     1080
ttgattgaga atgcgggccg ccaccgtgtc gctattttcca cctataccac tagcttaggt     1140
gccggtccta cctcgatctc tgcggtcggc gtactggctc cacactctgc ccttgccgtt     1200
cttgaggata ctattgatta ccccgcccggt gcccatactt ttgatgattt ttgcccggag     1260
tgccgtacct taggtttgca gggttgtgca ttccagtcta ctattgctga gctccagcgt     1320
ttaaaaatga aggtaggtaa aaccgggag tctgactaca aggacgacga tgacaagtaa     1380
taaggatcc

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<210> 197

<211> 74

<212> PRT

<213> Hepatitis E Virus

<220>

<223> z12-orf3-5'.pep

<223> Xaa = Unknown or Other at position 37

<400> 197

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Met Asn Asn Met Phe Cys Ala Ser Pro Met Gly Ser Pro Cys Ala Leu
 1          5          10          15
Gly Leu Phe Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro Arg
          20          25          30
His Arg Pro Ala Xaa Arg Leu Ala Ala Val Val Gly Gly Ala Ala Ala
          35          40          45
Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro Ser
          50          55          60
Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro
65          70

```

<210> 198

<211> 63

<212> DNA

<213> Hepatitis E Virus

<220>

<223> Primer orf23p

<400> 198

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acc

60

63

<210> 199

<211> 338

<212> PRT

<213> Hepatitis E Virus

<220>

<223> cksorf2m-2.pep

<400> 199

Glu	Phe	Met	Gly	Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala		
1				5					10					15			
Thr	Arg	Phe	Met	Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly		
			20					25					30				
Glu	Val	Gly	Arg	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr		
		35				40					45						
Leu	Leu	Gly	Gly	Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln		
	50					55				60							
Leu	Phe	Tyr	Ser	Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val		
65				70						75					80		
Lys	Leu	Tyr	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr		
				85				90						95			
Ile	Pro	His	Asp	Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp		
			100					105					110				
Tyr	Asp	Asn	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro		
		115					120					125					
Ser	Arg	Pro	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser		
	130					135					140						
Leu	Thr	Ala	Ala	Glu	Tyr	Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn		
145				150						155					160		
Pro	Met	Tyr	Val	Ser	Asp	Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly		
			165					170						175			
Ala	Gln	Ala	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp		
		180					185						190				
Gly	Arg	Pro	Leu	Thr	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val		
	195					200					205						
Leu	Pro	Leu	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys		
	210					215					220						
Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu		
225				230						235				240			
Ile	Glu	Asn	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr		
		245						250						255			
Ser	Leu	Gly	Ala	Gly	Pro	Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala		
		260					265						270				
Pro	His	Ser	Ala	Leu	Ala	Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala		
	275						280					285					
Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly		
	290					295					300						
Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu		
305				310						315				320			
Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Ser	Asp	Tyr	Lys	Asp	Asp	Asp		

Asp Lys
 325
330
335

<210> 200
 <211> 338
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> plorf2.2-6.pep

<400> 200

Glu	Phe	Met	Gly	Ala	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	1	5	10	15
Thr	Arg	Phe	Met	Lys	Asp	Leu	His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	20	25	30	
Glu	Val	Gly	Arg	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	35	40	45	
Leu	Leu	Gly	Gly	Leu	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	50	55	60	
Leu	Phe	Tyr	Ser	Arg	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	65	70	75	80
Lys	Leu	Tyr	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	85	90	95	
Ile	Pro	His	Asp	Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	100	105	110	
Tyr	Asp	Asn	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	115	120	125	
Ser	Arg	Pro	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	130	135	140	
Leu	Thr	Ala	Ala	Glu	Tyr	Asp	Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	145	150	155	160
Pro	Met	Tyr	Val	Ser	Asp	Thr	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	165	170	175	
Ala	Gln	Ala	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	180	185	190	
Gly	Arg	Pro	Leu	Thr	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val	195	200	205	
Leu	Pro	Leu	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	210	215	220	
Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	225	230	235	240
Ile	Glu	Asn	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	245	250	255	
Ser	Leu	Gly	Ala	Gly	Pro	Thr	Ser	Ile	Ser	Ala	Val	Gly	Val	Leu	Ala	260	265	270	
Pro	His	Ser	Ala	Leu	Ala	Val	Leu	Glu	Asp	Thr	Ile	Asp	Tyr	Pro	Ala	275	280	285	
Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Thr	Leu	Gly	290	295	300	
Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Ile	Ala	Glu	Leu	Gln	Arg	Leu	305	310	315	320
Lys	Met	Lys	Val	Gly	Lys	Thr	Arg	Glu	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	325	330	335	

Asp Lys

<210> 201
 <211> 37
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> Primer orf35p

<400> 201
 tatatgaatt catgaataac atgtcttttg catcgcc

37

<210> 202
 <211> 68
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> Primer orf33p

<400> 202
 tatatggatc cttattactt gtcacgctcg tccttgtagt cgcggcgcag accaagctgg
 ggcagatc

60

68

<210> 203
 <211> 132
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> pJOorf3-29.pep

<400> 203
 Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1 5 10 15
 Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys
 20 25 30
 Pro Arg His Arg Pro Ala Ser Arg Leu Ala Ala Val Val Gly Gly Ala
 35 40 45
 Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser
 50 55 60
 Pro Ser Pro Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met
 65 70 75 80
 Ser Phe His Asn Pro Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala
 85 90 95
 Pro Leu Ala Pro Leu Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Pro
 100 105 110
 Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Asp Tyr Lys Asp
 115 120 125
 Asp Asp Asp Lys
 130

<210> 204
 <211> 132
 <212> PRT
 <213> Hepatitis E Virus

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<220>

<223> plorf3-12.pep

<400> 204

Glu	Phe	Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys
1				5					10					15	
Ala	Leu	Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys
			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Ala
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
		50				55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75					80
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
			85						90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		
Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg	Asp	Tyr	Lys	Asp
		115					120					125			
Asp	Asp	Asp	Lys												
		130													

<210> 205

<211> 48

<212> DNA

<213> Hepatitis E Virus

<220>

<223> Primer orf23

<400> 205

ctcagcagtc ccatcagcac cgcggcgcag accaagctgg ggcagatc

48

<210> 206

<211> 459

<212> PRT

<213> Hepatitis E Virus

<220>

<223> CKSORF32M-3.pep

<400> 206

Glu	Phe	Met	Asn	Asn	Met	Ser	Phe	Ala	Ser	Pro	Met	Gly	Ser	Pro	Cys
1				5					10					15	
Ala	Leu	Gly	Leu	Phe	Cys	Cys	Cys	Ser	Ser	Cys	Phe	Cys	Leu	Cys	Cys
			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Val
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
		50				55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75					80
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
			85						90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		

```

Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg Arg Gly Ala Asp Gly
      115      120      125
Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu
      130      135      140
His Phe Ala Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala
145      150      155      160
Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr
      165      170      175
Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val
      180      185      190
Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu
      195      200      205
Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu
      210      215      220
Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln
225      230      235      240
Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
      245      250      255
Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Asp
      260      265      270
Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr
      275      280      285
Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser
      290      295      300
Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile
305      310      315      320
Gln Gln Tyr Ser Lys Thr Phe Tyr Val Leu Pro Leu Arg Gly Lys Leu
      325      330      335
Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr
      340      345      350
Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His
      355      360      365
Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr
      370      375      380
Ser Ile Ser Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val
385      390      395      400
Leu Glu Asp Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp
      405      410      415
Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln
      420      425      430
Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr
      435      440      445
Arg Glu Ser Asp Tyr Lys Asp Asp Asp Asp Lys
      450      455

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<210> 207

<211> 459

<212> PRT

<213> Hepatitis E Virus

<220>

<223> PLORF32M-14-5.pep

<400> 207

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Glu Phe Met Asn Asn Met Ser Phe Ala Ser Pro Met Gly Ser Pro Cys
 1      5      10      15
Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys

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			20					25					30		
Pro	Arg	His	Arg	Pro	Ala	Ser	Arg	Leu	Ala	Ala	Val	Val	Gly	Gly	Val
		35					40					45			
Ala	Ala	Val	Pro	Ala	Val	Val	Ser	Gly	Val	Thr	Gly	Leu	Ile	Leu	Ser
	50					55					60				
Pro	Ser	Pro	Ser	Pro	Ile	Phe	Ile	Gln	Pro	Thr	Pro	Ser	Pro	Pro	Met
65					70					75					80
Ser	Phe	His	Asn	Pro	Gly	Leu	Glu	Leu	Ala	Leu	Asp	Ser	Arg	Pro	Ala
				85					90					95	
Pro	Leu	Ala	Pro	Leu	Gly	Val	Thr	Ser	Pro	Ser	Ala	Pro	Pro	Leu	Pro
			100					105					110		
Pro	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Leu	Arg	Arg	Gly	Ala	Asp	Gly
		115					120					125			
Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	Asp	Leu
	130					135					140				
His	Phe	Ala	Gly	Thr	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	Ile	Ala
145					150					155					160
Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	Pro	Thr
				165					170					175	
Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	Pro	Val
			180					185					190		
Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val	Glu
		195					200					205			
Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Thr	Ile	Pro	His	Asp	Ile	Asp	Leu
	210					215					220				
Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu	Gln
225					230					235					240
Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val	Leu
				245					250					255	
Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr	Asp
			260					265					270		
Gln	Thr	Thr	Tyr	Gly	Ser	Ser	Thr	Asn	Pro	Met	Tyr	Val	Ser	Asp	Thr
		275					280					285			
Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg	Ser
	290					295					300				
Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Thr	Thr	Ile
305					310					315					320
Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Tyr	Val	Leu	Pro	Leu	Arg	Gly	Lys	Leu
				325					330					335	
Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn	Tyr
			340					345					350		
Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala	Gly	His
		355					360					365			
Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly	Pro	Thr
	370														

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<211> 36
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Primer orf2mid5p

<400> 208
tatatgaatt catgggtgct gatgggactg ctgagc 36

<210> 209
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 1440o1.seq

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 209
ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gcc aat 47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1             5             10             15

tcc gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtt 95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
          20             25             30

caa act gat atc ctt att aac ctg atg caa ccc cgt cag ctt gtg ttc 143
Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
          35             40             45

cgg cct gaa gtt ctc tgg aac cat ccg atc cag cga gtt ata cat aat 191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
          50             55             60

gag ctg gaa caa tac tgt cga gcc cgc gct ggc cgc tgt ctt gag gtg 239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
          65             70             75

ggc gct cac cca agg tct att aat gat aac ccc aat gtt ctg cac cgg 287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
          80             85             90             95

tgc ttt ctc cgc ccg gtt ggg aga gac gtc cag cgc tgg tat tcc gcc 335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
          100             105             110

ccc act cgt ggt cca gcg gct aac tgc cgc cgt tct gcg cta cgc ggt 383

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Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
115 120 125

ttg ccc cct gtc gac cgc act tac tgt yty gat gg
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130 135

418

<210> 210
<211> 138
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 210
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
1 5 10 15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
20 25 30
Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
35 40 45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
50 55 60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
65 70 75 80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
85 90 95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
100 105 110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115 120 125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130 135

<210> 211
<211> 197
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 1440o2.seq

<221> CDS
<222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

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```
<400> 211
g aca gaa ttr att tcg tcg gct gga ggt caa ctg ttc tac tcc cgc ccg      49
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1              5              10              15

ggt gtc tca gcc aat ggc gag ccg act gtt aag tta tac acc tct gtc      97
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
          20              25              30

gag aat gca cag cag gat aag ggc att gct ata cca cat gat ata gac      145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
          35              40              45

tta ggg gat tcc cgt gtg gtt ata caa gat tat gay aac car cay gaa      193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
          50              55              60

caa g
Gln
65      197
```

```
<210> 212
<211> 65
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63
```

```
<400> 212
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1              5              10              15
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
          20              25              30
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
          35              40              45
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
          50              55              60
Gln
65
```

```
<210> 213
<211> 418
<212> DNA
<213> Hepatitis E Virus
```

```
<220>
<223> 2015-1.seq
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```
<221> CDS
<222> (3)...(416)
```

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 213

```

ct ggc aty act act gcy att gag cag gct gct ctg gct gcg gct aac      47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1             5             10             15

tct gcc ttg gcg aat gct gtg gtg gtc cgg ccg ttc ctg tcc cgc act      95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr
                20             25             30

cag act gat att ctt att aat ttg atg caa ccc cgg caa ctt gta ttc      143
Gln Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
                35             40             45

cgc cct gag gtt ttg tgg aac cat ccg atc cag cga gtc ata cat aat      191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
                50             55             60

gag ctg gag cag tat tgc cgt gct cgt gct ggt cgc tgc ctg gag gtt      239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
                65             70             75

ggg gct cat cca aga tct atc aat gac aac cct aat gtt ctg cac cgg      287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
                80             85             90             95

tgt ttc ctc cgt ccg gtt ggg cga gac gta cag cgt tgg tat tct gcc      335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
                100             105             110

cct act cgc ggc ccg gcg gct aat tgc cgc cgt tcc gcg tta cgt ggc      383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
                115             120             125

cta cct cct gtc gac cgc act tac tgt yty gat gg                      418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
                130             135

```

<210> 214

<211> 138

<212> PRT

<213> Hepatitis E Virus

<220>

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 214

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```

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
 1          5          10          15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Thr Gln
 20          25          30
Thr Asp Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
 35          40          45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
 50          55          60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
 65          70          75          80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
 85          90          95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
100          105          110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115          120          125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130          135

```

<210> 215
 <211> 197
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 2015o2.seq
 <221> CDS
 <222> (2)...(196)

<223> Xaa = Unknown or Other at position 3
 <223> Xaa = Unknown or Other at position 60
 <223> Xaa = Unknown or Other at positions 62-63

```

<400> 215
g aca gaa ttr att tcg tcg gct gga ggc cag ctc ttc tac tcc cgc cca      49
  Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
  1          5          10          15

gtc gtc tca gcc aat ggc gag ccg act gtt aaa ttg tat aca tcc gtc      97
Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20          25          30

gag aat gcg cag cag gac aag ggc att gcc ata cca cat gat ata gat      145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35          40          45

cta gga gat tcc cgc gtg gtt atc cag gat tat gay aac car cay gaa      193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50          55          60

caa g      197
Gln
65

```

<210> 216
 <211> 65
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 3
 <223> Xaa = Unknown or Other at position 60
 <223> Xaa = Unknown or Other at positions 62-63

<400> 216
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60
 Gln
 65

<210> 217
 <211> 251
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 14404-2.seq

<221> CDS
 <222> (3)...(251)
 <223> orf2

<223> orf3 from position 1 to position 165

<400> 217
 at att cat cca acc aac ccc ttt gcc tcc gac gtc gta tcg caa tcc 47
 Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser
 1 5 10 15
 ggg gct gga gct cgc cct cga cag ccg gcc cgc ccc ctc ggc tcc tct 95
 Gly Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser
 20 25 30
 tgg cgt gac cag tcc cag cgc ccc ccc gct gtc ccc cgt cgt cga tct 143
 Trp Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Arg Ser
 35 40 45
 acc cca act ggg gct gcg ccg cta act gct gtt tca cca gcg cct gat 191
 Thr Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp
 50 55 60
 acg gcc cca gtc cct gat gtt gac tct cgt ggc gct atc ttg cgc cgg 239

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Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg
65 70 75

cag tat aac cta
Gln Tyr Asn Leu
80

251

<210> 218
<211> 83
<212> PRT
<213> Hepatitis E Virus

<400> 218
Ile His Pro Thr Asn Pro Phe Ala Ser Asp Val Val Ser Gln Ser Gly
1 5 10 15
Ala Gly Ala Arg Pro Arg Gln Pro Ala Arg Pro Leu Gly Ser Ser Trp
20 25 30
Arg Asp Gln Ser Gln Arg Pro Pro Ala Val Pro Arg Arg Ser Thr
35 40 45
Pro Thr Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr
50 55 60
Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
65 70 75 80
Tyr Asn Leu

<210> 219
<211> 55
<212> PRT
<213> Hepatitis E Virus

<220>
<223> 14404-2.seq orf3

<400> 219
Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr Arg Asn Pro
1 5 10 15
Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu
20 25 30
Gly Val Thr Ser Pro Ser Ala Pro Pro Leu Ser Pro Val Val Asp Leu
35 40 45
Pro Gln Leu Gly Leu Arg Arg
50 55

<210> 220
<211> 251
<212> DNA
<213> Hepatits E Virus

<220>
<223> 20154-2.seq

<221> CDS
<222> (3)...(251)
<223> orf2

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<223> orf3 from position 1 to position 165

<400> 220

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at att cat cca acc aac ccc ttt gcc gcc gac gtc gta tca caa ccc      47
  Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro
    1              5              10              15

ggg gct gga gct cgc cct cga cag ccg ccc cgc ccc ctc ggc tcc tct      95
Gly Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser
          20              25              30

tgg cgt gat cag tcc cag cgc ccc tcc gct gcc ccc cgt cgt cga tct      143
Trp Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser
          35              40              45

acc cca gct ggg gct gcg ccg tta act gct gtt tcc cct gcg ccc gat      191
Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp
          50              55              60

acg gcc cca gtc ccc gac gtt gat tcc cgt ggt gcc atc ctg cgc cgg      239
Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg
          65              70              75

cag tat aac cta      251
Gln Tyr Asn Leu
  80
```

<210> 221

<211> 83

<212> PRT

<213> Hepatitis E Virus

<400> 221

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Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser Gln Pro Gly
  1              5              10              15
Ala Gly Ala Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly Ser Ser Trp
          20              25              30
Arg Asp Gln Ser Gln Arg Pro Ser Ala Ala Pro Arg Arg Arg Ser Thr
          35              40              45
Pro Ala Gly Ala Ala Pro Leu Thr Ala Val Ser Pro Ala Pro Asp Thr
          50              55              60
Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
          65              70              75              80
Tyr Asn Leu
```

<210> 222

<211> 55

<212> PRT

<213> Hepatitis E Virus

<220>

<223> 20154-2.seq orf3

<400> 222

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Ile Phe Ile Gln Pro Thr Pro Leu Pro Pro Thr Ser Tyr His Asn Pro
```

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1 5 10 15
Gly Leu Glu Leu Ala Leu Asp Ser Arg Pro Ala Pro Ser Ala Pro Leu
20 25 30
Gly Val Ile Ser Pro Ser Ala Pro Pro Leu Pro Pro Val Val Asp Leu
35 40 45
Pro Gln Leu Gly Leu Arg Arg
50 55

<210> 223
<211> 48
<212> PRT
<213> Hepatitis E Virus

<220>
<223> US-2 3-2e

<400> 223
Thr Ile Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
1 5 10 15
Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
20 25 30
Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser
35 40 45

<210> 224
<211> 33
<212> PRT
<213> Hepatitis E Virus

<220>
<223> US-2 4-2

<400> 224
Asp Ser Arg Pro Ala Pro Leu Val Pro Leu Gly Val Thr Ser Pro Ser
1 5 10 15
Ala Pro Pro Leu Pro Pro Val Val Asp Leu Pro Gln Leu Gly Leu Arg
20 25 30
Arg

<210> 225
<211> 450
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 5p.pile {hpesvp}

<400> 225
ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgcctt 60
ggcgaatgct gtggtagtta ggccttttct ctctcaccag cagattgaga tcctcattaa 120
cctaatagcaa cctcgccagc ttgttttccg ccccgagggt ttctggaatc atcccatcca 180
gcgtgtcatc cataacgagc tggagcttta ctgccgcgcc cgctccggcc gctgtcttga 240
aattggcgcc catccccgct caataaatga taatcctaata gtggtccacc gctgcttcct 300
ccgccctggt gggcggtgatg ttcagcgctg gtatactgct cccactcgcg ggccggctgc 360
taattgccgg cgttccgcgc tgcgcgggct tcccgctgct gaccgcactt actgcctcga 420
cgggttttct ggctgtaact ttcccgcgca 450

<210> 226
 <211> 450
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 5p.pile {hpeuigh}

<400> 226
 ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca attctgccct 60
 tgcgaatgct gtggtagtta ggctttttct ctctcaccag cagattgaga tccttattaa 120
 cctaatagcaa cctcgccagc ttgttttccg ccccgagggt ttctggaacc accccatcca 180
 gcgtgtcatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgccttga 240
 aattggtgcc caccctcgct caataaacga caatcctaata gtggtccacc gctgcttcct 300
 ccgccctgcc gggcgtgatg ttcagcgttg gtatactgct cctaccgcgc ggccggtgc 360
 taattgccgg ggttcgcgcac tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420
 cgggttttct ggctgtaact ttcccgcga 450

<210> 227
 <211> 450
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 5p.pile {hpea}

<400> 227
 ggctcctggc atcactactg ctattgagca ggctgctcta gcagcggcca actctgccct 60
 tgcgaatgct gtggtagtta ggctttttct ctctcaccag cagattgaga tccttattaa 120
 cctaatagcaa cctcgccagc ttgttttccg ccccgagggt ttctggaacc atcccatcca 180
 gcgtgttatc cataatgagc tggagcttta ctgtcgcgcc cgctccggcc gctgcctcga 240
 aattggtgcc ccccccgct caataaatga caatcctaata gtggtccacc gttgcttcct 300
 ccgtcctgcc gggcgtgatg ttcagcgttg gtatactgcc cctaccgcgc ggccggtgc 360
 taattgccgg cggttcgcgc tgcgcgggct ccccgctgct gaccgcactt actgcttcga 420
 cgggttttct ggctgtaact ttcccgcga 450

<210> 228
 <211> 446
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 5p.pile {840455p}

<400> 228
 cctggcatta ctactgccat tgagcaggct gctctggctg cggccaattc tgccttggcg 60
 aatgctgtgg tggttcggcc gtttttatct cgcgtgcaaa ccgagattct tattaatttg 120
 atgcaacccc ggcagttggt ttccgcctt gaggtacttt ggaatcacc tatccagcgg 180
 gttatacata atgaattaga acagtactgc cgggctcggg ctggtcggtt cttggagggt 240
 ggagctcacc caagatccat taatgacaac cccaacgttc tgcacgggtg ttcccttaga 300
 ccggttggcc gagatgttca gcgctggtac tctgccccca ccgcggccc tgcgggtaat 360
 tgcgcgcgct ccgcgttgcg tggctcccc cccgctgacc gcacttactg ctttgatgga 420
 ttctcccggt gtgcttttgc tgcaga 446

<210> 229
 <211> 450

<212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 5p.pile {hpenssp}

<400> 229
 ggctcctggc atcactactg ctattgagca agcagctcta gcagcggcca actccgccct 60
 tgcgaatgct gtggtgggtcc ggccttttct tccccatcag cagggttgaga tccttataaa 120
 tctcatgcaa cctcggcagc tgggtgttctg tcttgagggt ttttggaatc acccgattca 180
 acgtgttata cataatgagc ttgagcagta ttgccgtgct cgctcggggtc gctgccttga 240
 gattggagcc caccacgct ccattaatga taatcctaata gtcctccatc gctgctttct 300
 ccaccccgct gcccgggatg ttcagcgctg gtacacagcc ccgactaggg gacctgcggc 360
 gaactgtcgc cgctcggcac ttcggtgtct gccaccagcc gaccgcactt actgttttga 420
 tggctttgccc ggctgcggtt ttgccgcca 450

<210> 230
 <211> 450
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 5p Consensus

<221> variation
 <222> (1)...(450)
 <223> n = a or g or c or t/u, unknown or other in each instance and is indicated in Figure 9

<400> 230
 nnnncctggc atnactactg cnattgagca ngcngctctn gcngcggcca antcngccnt 60
 ngcgaatgct gtggtngtnn ggcntttnt ntncnnnnng cannnngaga tncnatnaa 120
 nntnatgcaa ccncgncagn tngtnttncg nccngaggtn ntntggaanc anccnatnca 180
 ncngtgnatn cataangann tngancnnta ntgncngcn cgnnnnggnc gntgnntnga 240
 nnttgngcn canccnngnt cnatnaanga naanccnaan gtntntcanc gntgnttnt 300
 nnnccngnn ggncngnatg ttcagcgntg gtannngcn ccnncnngng gncngcngc 360
 naantgncn ngntcngcn tncngngnt nccnncngcn gaccgcactt actgnntnga 420
 nggnttnncn ngntgnnnnt ttncngcnga 450

<210> 231
 <211> 300
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 3p.pile {hpea} shown in Figure 9B

<400> 231
 actgagtcag tgaagccagt gcttgacctg acaaattcaa ttctgtgtcg ggtggaatga 60
 ataacatgct ttttgctgcg cccatgggtt cgcgaccatg cgccctcggc ctattttgct 120
 gttgctcctc atgtttctgc ctatgctgcc cgcgccaccg cccggtcagc cgtctggccg 180
 ccgtcgtggg cggcgcagcg gcggttccgg cgggtggttc tggggtgacc ggggttgattc 240
 tcagcccttc gcaatccctt atattcatcc aaccaacccc ttgcgcccg atgtcaccgc 300

<210> 232
 <211> 300
 <212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpeuigh} shown in Figure 9B

<400> 232

actgagtcgg	tgaagccagt	gctcgacttg	acaaattcaa	tcctgtgtcg	ggtggaatga	60
ataacatgtc	ttttgctgcg	cccatgggtt	ggcgaccatg	cgccctcggc	ctattttgct	120
gttgctcctc	atgtttctgc	ctatcgtgcc	cgcgccaccg	cccggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggttccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatccct	atattcatcc	aaccaacccc	ttcgcccccg	atgtcaccgc	300

<210> 233

<211> 300

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpesvp} shown in Figure 9B

<400> 233

actgagtcag	taaaaccagt	gctcgacttg	acaaattcaa	tcttgtgtcg	ggtggaatga	60
ataacatgtc	ttttgctgcg	cccatgggtt	cgcgaccatg	cgccctcggc	ctattttgtt	120
gctgctcctc	atgtttttgc	ctatgctgcc	cgcgccaccg	cccggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggttccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatccct	atattcatcc	aaccaacccc	ttcgcccccg	atgtcaccgc	300

<210> 234

<211> 300

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {hpenssp} shown in Figure 9B

<400> 234

acagagtctg	ttaagcctat	acttgacctt	acacactcaa	ttatgcaccg	gtctgaatga	60
ataacatgtg	gtttgctgcg	cccatgggtt	cgccaccatg	cgccctaggc	ctcttttctt	120
gttgctcctc	ttgtttctgc	ctatgttgcc	cgcgccaccg	accggtcagc	cgtctggccg	180
ccgtcgtggg	cggcgcagcg	gcggtaccgg	cggtggtttc	tggggtgacc	gggttgattc	240
tcagcccttc	gcaatccct	atattcatcc	aaccaacccc	tttgccccag	acgttgccgc	300

<210> 235

<211> 297

<212> DNA

<213> Hepatitis E Virus

<220>

<223> 3p.pile {840453p} shown in Figure 9B

<400> 235

acagagacta	ttaaacctgt	acttgatctc	acaaattcca	tcatacagcg	ggtggaatga	60
ataacatgtc	ttttgcatcg	cccatgggat	caccatgcgc	cctagggctg	ttctgttggt	120
gttctcatg	tttctgccta	tgtgcccgc	gccaccggcc	ggtcagccgt	ctggccgctg	180
ccgtgggcgg	cgcagcggcg	gtgccggcgg	tggtttctgg	agtgacaggg	ttgattctca	240
gcccttcgcc	ctcccctata	ttcatccaac	caacccttc	gccgccgatg	tcgttttc	297

<210> 236
 <211> 300
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 3p Consensus shown in Figure 9B

<221> variation
 <222> (3)...(300)
 <223> n = a or g or c or t/u, unknown or other in each instance and is indicated in Figure 9B

<400> 236

acngagncnn	tnaanccnnt	nctngannntn	acanantcna	tnntnnnnncg	gnnngaata	60
ataacatgtn	ntttgennncg	cccatgggnt	nnnnaccatg	cgccctnggn	ctnttntgnt	120
gntgntcctc	ntgtttntgc	ctatnntgcc	cgcgccaccg	nccggtcagc	cgtctggccg	180
ncgncgtggg	cggcgcagcg	gcggtncggg	cggtgggttc	tggngtgacn	gggttgattc	240
tcagcccttc	genntccct	atattcatcc	aaccaacccc	ttngccncng	angtnnnnnc	300

<210> 237
 <211> 250
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 3p.pile {hpea} shown in Figure 9C

<400> 237

agcgcttacc	ctgtttaacc	ttgctgacac	cctgcttggc	ggctctaccga	cagaattgat	60
ttcgctcggct	gggtggccagc	tggtctactc	tcgccccgtc	gtctcagcca	atggcgagcc	120
gactgttaag	ctgtatacat	ctgtggagaa	tgctcagcag	gataagggta	ttgcaatccc	180
gcatgacatc	gacctcgggg	aatcccgtgt	agttattcag	gattatgaca	accaacatga	240
gcaggaccga						250

<210> 238
 <211> 250
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 3p.pile {hpeuigh} shown in Figure 9C

<400> 238

agcgcttacc	ctgtttaacc	ttgctgacac	cctgcttggc	ggctctaccga	cagaattgat	60
ttcgctcggct	gggtggccagc	tggtctactc	tcgccccgtc	gtctcagcca	atggcgagcc	120
gactgttaag	ctgtatacat	ctgtagagaa	tgctcagcag	gataagggta	ttgcaatccc	180
gcatgacatc	gacctcgggg	aatctcgagt	tgttattcag	gattatgaca	accaacatga	240
gcaggaccg						250

<210> 239
 <211> 250
 <212> DNA
 <213> Hepatitis E Virus

<220>
 <223> 3p.pile {hpesvp} shown in Figure 9C

<400> 239
agccctcacc ctgttcaacc ttgctgacac tctgcttggc ggccctgccga cagaattgat 60
ttcgtcggct ggtggccagc tgttctactc ccgtcccgtt gtctcagcca atggcgagcc 120
gactgttaag ttgtatacat ctgtagagaa tgctcagcag gataagggta ttgcaatccc 180
gcatgacatt gacctcggag aatctcgtgt ggttattcag gattatgata accaacaatga 240
acaagatcgg 250

<210> 240
<211> 250
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 3p.pile {hpenssp} shown in Figure 9C

<400> 240
agctctaaca ttacttaacc ttgctgacac gctcctcggc gggctcccga cagaattaat 60
ttcgtcggct ggcgggcaac tgttttattc ccgcccgggt gtctcagcca atggcgagcc 120
aaccgtgaag ctctatacat cagtggagaa tgctcagcag gataagggtg ttgctatccc 180
ccacgatatc gatcttgggtg attcgcgtgt ggtcattcag gattatgaca accagcatga 240
gcaggatcgg 250

<210> 241
<211> 250
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 3p.pile {840453p} shown in Figure 9C

<400> 241
tgccctgact ctgtttaatc ttgctgatac gcttcttgggt ggtttaccga cagaattgat 60
ttcgtcggct ggggggtcaac tgttttactc ccgccctggt cagaattgat ttcgtcggct 120
gggggtcaac tgttttactc ccgccctggt tgccgagcaa gacaagggca tcaccattcc 180
acacgacata gatttaggtg actcccgtgt ggttatccag gattatgata accagcacga 240
acaagatcga 250

<210> 242
<211> 250
<212> DNA
<213> Hepatitis E Virus

<220>
<223> 3p Consensus shown in Figure 9C

<221> variation
<222> (1)...(250)
<223> n = a or g or c or t/u, unknown or other at each
instance and is indicated in Figure 9C

<400> 242
ngcnctnact ntnntnaanc ttgctganac nctnctnggn ggnntnccga cagaattnat 60
ttcgtcggct ggnngncanc tgtntantc ncgnccngtn gtctcngcca atggcgagcc 120
nacngtnaag ntnntanacat cngtnagagaa tgcnacgcan ganaaggggn tnnctatncc 180
ncanganatn ganntnggng antcncngnt ngtnatncag gattatgana accancanga 240
ncanganecgn 250

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<210> 243
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Aulol-wlabolpl.pat

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 243
ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aat      47
  Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    1             5             10             15

tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg      95
  Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
                20             25             30

cag act gag atc ctt att aac ttg atg caa cct cgg cag ctg gtg ttc      143
  Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
                35             40             45

cga cct gag gtg ctt tgg aat cat ccc att cag cgg gtt atc cat aat      191
  Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
                50             55             60

gag tta gaa caa tac tgc cgg gcc cgg gcc ggc cgt tgc cta gag gtg      239
  Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
                65             70             75

ggg gcc cac cca agg tcc att aac gat aac ccc aat gtt ttg cac cgg      287
  Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
                80             85             90             95

tgt ttt ctg cga ccg gtc ggg agg gat gtt cag cgc tgg tac tct gcc      335
  Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
                100            105            110

ccc acc cgc ggc cct gcg gct aac tgc cgc cgc tcc gct ttg cgt ggc      383
  Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
                115            120            125

ctt ccc ccc gtc gac cgc act tac tgt yty gat gg                      418
  Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
                130            135

```

<210> 244

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<211> 138
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

<400> 244
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
1 5 10 15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
20 25 30
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg
35 40 45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
50 55 60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
65 70 75 80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
85 90 95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
100 105 110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
115 120 125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
130 135

<210> 245
<211> 197
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Aulo2-wlao2.pat

<221> CDS
<222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 17

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 245
g aca gaa ttr att tgc tgc gct ggg gga cag tta ttc tac tcc cgc cct 49
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
1 5 10 15

gty gtc tca gcc aat ggc gag ccg act gtt aaa tta tat aca tct gta 97
Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val

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                20                25                30
gag aat gcg cag cag gac aag ggg att gcc atc cca cat gat ata gat      145
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
                35                40                45

ctg ggc gac tct cgt gtg gtg atc cag gat tat gay aac car cay gaa      193
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
                50                55                60

caa g
Gln
65

```

197

```

<210> 246
<211> 65
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 17

<223> xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

```

```

<400> 246
Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1          5          10          15
Xaa Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
          20          25          30
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
          35          40          45
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
          50          55          60
Gln
65

```

```

<210> 247
<211> 418
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Ar1o1-f73o1p1.pat

<221> CDS
<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 137

```

<400> 247

ct ggc aty act act gcy att gag caa gct gct ctg gct gcg gcc aac	47
Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn	
1 5 10 15	
tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tcc cgt gtg	95
Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val	
20 25 30	
cag acc gag att ctt att aac cta atg caa ccc cgg cag ctg gtt ttt	143
Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe	
35 40 45	
cgt cct gag gtg ctt tgg aac cat cct atc cag cgg gtt att cat aat	191
Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn	
50 55 60	
gag tta gaa cag tac tgt cgg gct cgg gct ggt cgc tgc cta gag gtc	239
Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val	
65 70 75	
ggg gcc cac cca agg tcc att aat gat aac cct aat gtt ttg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg	
80 85 90 95	
tgc ttc cta cga cca gtc ggg agg gat gtt caa cgt tgg tat tcc gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc acc cgc ggt cct gct gcc aac tgc cgc cgt tcc gct ctg cgc ggc	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc cct ccc gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 248
 <211> 138
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 2
 <223> Xaa = Unknown or Other at position 5
 <223> Xaa = Unknown or Other at position 137

<400> 248

Gly Xaa Thr Thr Xaa Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser
1 5 10 15
Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val Gln
20 25 30
Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg

113/117

```

      35              40              45
Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu
  50              55              60
Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val Gly
  65              70              75              80
Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg Cys
      85              90              95
Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala Pro
      100              105              110
Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly Leu
      115              120              125
Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp
  130              135
```

<210> 249
<211> 145
<212> DNA
<213> Hepatitis E Virus

<220>
<223> Ar1-f73o2p2.pat

<221> CDS
<222> (1)...(144)

<223> Xaa = Unknown or Other at position 1
<223> Xaa = Unknown or Other at position 3
<223> Xaa = Unknown or Other at position 44
<223> Xaa = Unknown or Other at positions 46-47

```

<400> 249
gtg gtc tcr gcc aat ggc gag ccg act gtt aag cta tat aca tct gta      48
Xaa Val Xaa Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
  1              5              10              15

gag aac gcg cag cag gat aaa ggg atc gcc att cca cac gat ata gat      96
Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
      20              25              30

ctg ggc gat tcc cgt gtg gtc att cag gat tat gay aac car cay gaa      144
Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
      35              40              45

c                                                                    145
```

<210> 250
<211> 48
<212> PRT
<213> Hepatitis E Virus

<220>
<223> Xaa = Unknown or Other at position 1
<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 44

<223> Xaa = Unknown or Other at positions 46-47

<400> 250

Xaa	Val	Xaa	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
1				5					10					15	
Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile	Asp
			20					25					30		
Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Xaa	Asn	Xaa	Xaa	Glu
		35					40					45			

<210> 251

<211> 418

<212> DNA

<213> Hepatitis E Virus

<220>

<223> Ar2ol-f77olpl.pat

<221> CDS

<222> (3)...(416)

<223> Xaa = Unknown or Other at position 2

<223> Xaa = Unknown or Other at position 5

<223> Xaa = Unknown or Other at position 41

<223> Xaa = Unknown or Other at position 44

<223> Xaa = Unknown or Other at position 93

<223> Xaa = Unknown or Other at position 137

<400> 251

ct	ggc	aty	act	act	gcy	att	gag	caa	gct	gct	ctg	gct	gcg	gct	aac	47
	Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	
1					5						10				15	
tct	gcc	ttg	gcy	aat	gct	gtg	gtg	ggt	cgg	ccg	ttt	cta	tcc	cgt	gtg	95
Ser	Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	
				20					25					30		
cag	act	gag	atc	ctt	att	aac	tta	atg	car	ccc	cgg	car	ctg	ggt	ttc	143
Gln	Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Xaa	Pro	Arg	Xaa	Leu	Val	Phe	
			35					40					45			
cgt	ccc	gag	gtg	ctt	tgg	aat	cat	ccc	att	caa	cgg	ggt	att	cat	aat	191
Arg	Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	
			50				55					60				
gaa	tta	gag	cag	tac	tgc	cgg	acc	cgg	gct	ggc	cgt	tgt	tta	gag	gtc	239
Glu	Leu	Glu	Gln	Tyr	Cys	Arg	Thr	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	
			65				70					75				

115/117

gga gcc cat cca agg tcc att aat gac aac cct aac gtt cyg cac cgg	287
Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Xaa His Arg	
80 85 90 95	
tgc ttc tta cga cca gtc ggg agg gat gtc caa cga tgg tac tca gcc	335
Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala	
100 105 110	
ccc act cgc ggc cct gcg gct aat tgc cgt cgt tcc gct ttg cgt ggt	383
Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly	
115 120 125	
ctc cct cct gtc gac cgc act tac tgt yty gat gg	418
Leu Pro Pro Val Asp Arg Thr Tyr Cys Xaa Asp	
130 135	

<210> 252
 <211> 138
 <212> PRT
 <213> Hepatitis E Virus

<220>
 <223> Xaa = Unknown or Other at position 2
 <223> Xaa = Unknown or Other at position 5
 <223> Xaa = Unknown or Other at position 41
 <223> Xaa = Unknown or Other at position 44
 <223> Xaa = Unknown or Other at position 93
 <223> Xaa = Unknown or Other at position 137

<400> 252																	
Gly	Xaa	Thr	Thr	Xaa	Ile	Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser		
1				5					10					15			
Ala	Leu	Ala	Asn	Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	Arg	Val	Gln		
			20					25					30				
Thr	Glu	Ile	Leu	Ile	Asn	Leu	Met	Xaa	Pro	Arg	Xaa	Leu	Val	Phe	Arg		
		35					40					45					
Pro	Glu	Val	Leu	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu		
	50					55					60						
Leu	Glu	Gln	Tyr	Cys	Arg	Thr	Arg	Ala	Gly	Arg	Cys	Leu	Glu	Val	Gly		
65					70					75					80		
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Xaa	His	Arg	Cys		
				85				90						95			
Phe	Leu	Arg	Pro	Val	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Ser	Ala	Pro		
			100					105					110				
Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu		
		115					120					125					
Pro	Pro	Val	Asp	Arg	Thr	Tyr	Cys	Xaa	Asp								
		130				135											

<210> 253
 <211> 197

<212> DNA
 <213> Hepatitis E Virus

<220>
 <223> Ar2o2-f7702.pat

<221> CDS
 <222> (2)...(196)

<223> Xaa = Unknown or Other at position 3

<223> Xaa = Unknown or Other at position 60

<223> Xaa = Unknown or Other at positions 62-63

<400> 253
 g aca gaa ttr att tcg tcg gct ggg ggt cag ttg ttt tac tcc cgc cct 49
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15
 gtc gtc tca gcc aat ggc gag ccg act gtt aag ttg tat aca tct gtg 97
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30
 gag aat gcg cag cag gat aaa gga atc gcc atc cca cac gac ata gat 145
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45
 ctg ggc gat tcc cgt gtg gtt att cag gat tat gay aac car cay gaa 193
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu
 50 55 60
 caa g 197
 Gln
 65

<210> 254
 <211> 65
 <212> PRT
 <213> Hepatits E Virus

<220>
 <223> Xaa = Unknown or Other at position 3
 <223> Xaa = Unknown or Other at position 60
 <223> Xaa = Unknown or Other at positions 62-63

<400> 254
 Thr Glu Xaa Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 1 5 10 15
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 20 25 30
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 35 40 45
 Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Xaa Asn Xaa Xaa Glu

Gln 65	50	55	60
		<210> 255 <211> 23 <212> DNA <213> Hepatits E Virus <220> <223> HEVConsORF 1N-a1 <400> 255 ccrtcrarrc artaggtgcg gtc	23
		<210> 256 <211> 25 <212> DNA <213> Hepatits E Virus <220> <223> HEVConsORF 2N-a1 <400> 256 cytgytcrtg ytggttrtca taatc	25
		<210> 257 <211> 21 <212> DNA <213> Hepatits E Virus <220> <223> HEVConsORF 1N-s2 <400> 257 cygccytkgc gaatgctgtg g	21
		<210> 258 <211> 25 <212> DNA <213> Hepatits E Virus <220> <223> HEVConsORF 2N-a2 <400> 258 gytcrtygtg rtrtrcataa tcctg	25